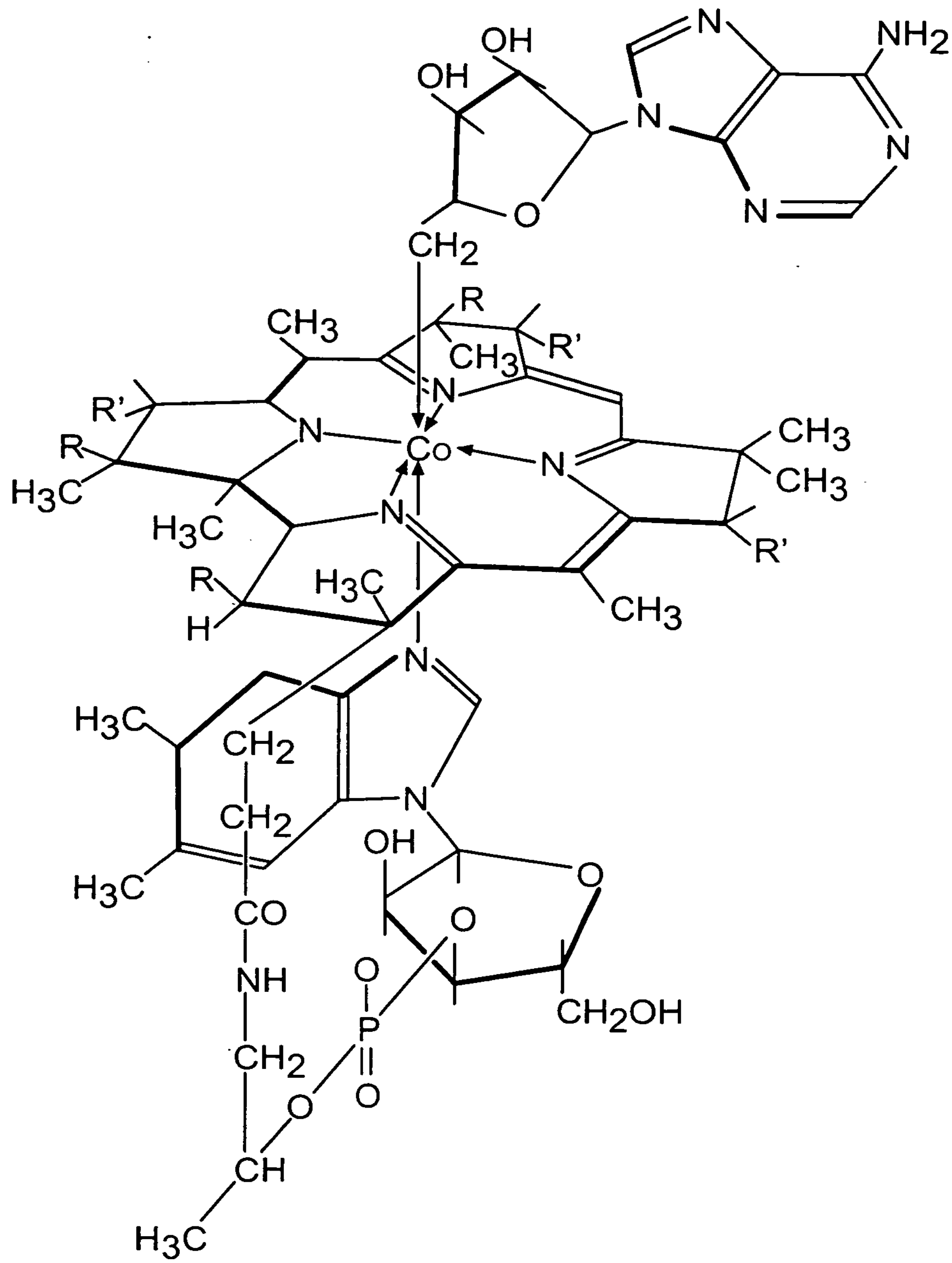


ADENOSYLCOBALAMIN R = CH_2COHN_2, R' = $CH_2CH_2CONH_2$

FIG. 1

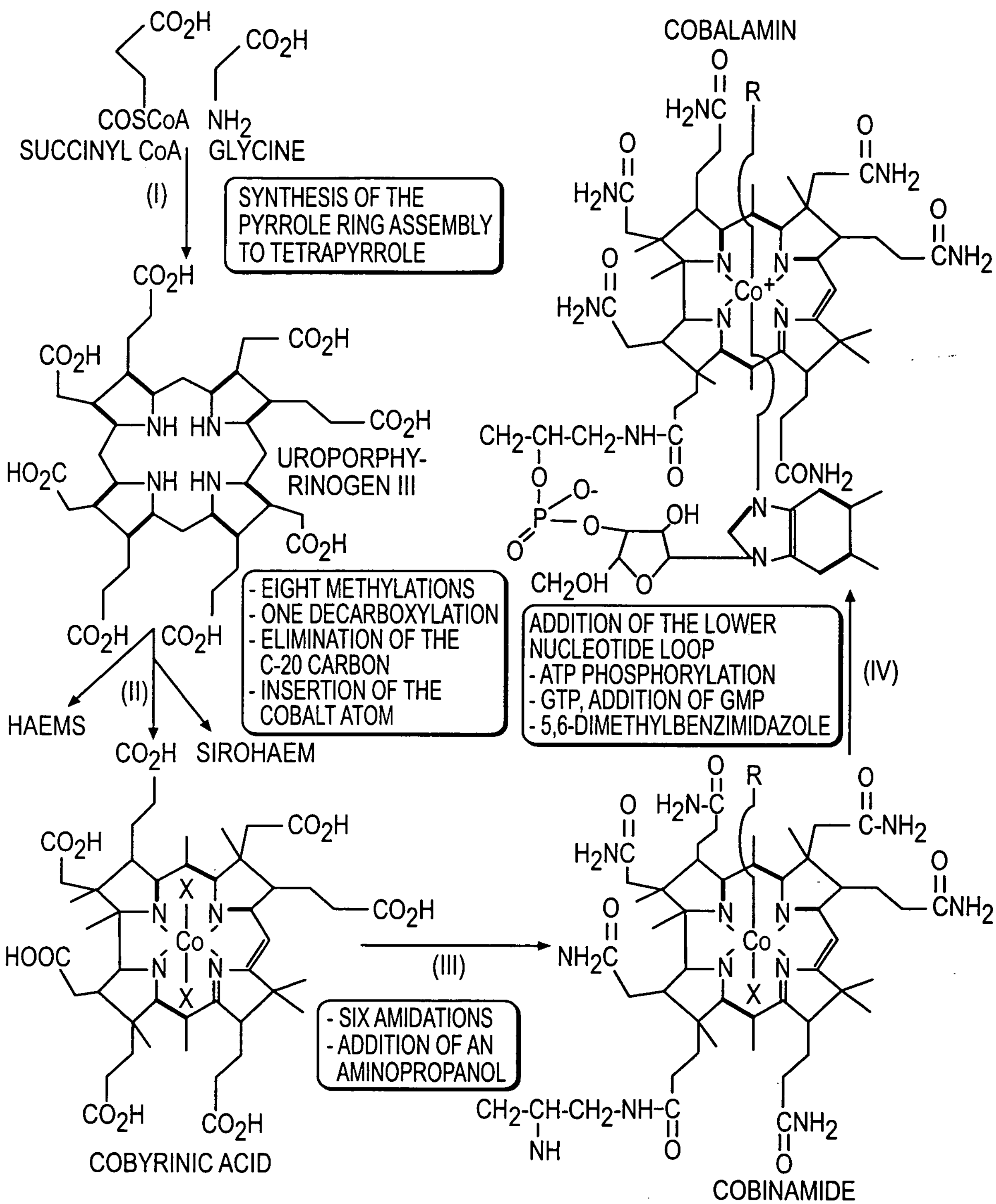

SUCCINYL CoA
GLYCINE
(I)
SYNTHESIS OF THE PYRROLE RING ASSEMBLY TO TETRAPYRROLE
UROPORPHYRINOGEN III
- EIGHT METHYLATIONS
- ONE DECARBOXYLATION
- ELIMINATION OF THE C-20 CARBON
- INSERTION OF THE COBALT ATOM
(II)
HAEMS
SIROHAEM
COBYRINIC ACID
(III)
- SIX AMIDATIONS
- ADDITION OF AN AMINOPROPANOL
COBINAMIDE
(IV)
ADDITION OF THE LOWER NUCLEOTIDE LOOP
- ATP PHOSPHORYLATION
- GTP, ADDITION OF GMP
- 5,6-DIMETHYLBENZIMIDAZOLE
COBALAMIN

FIG. 2

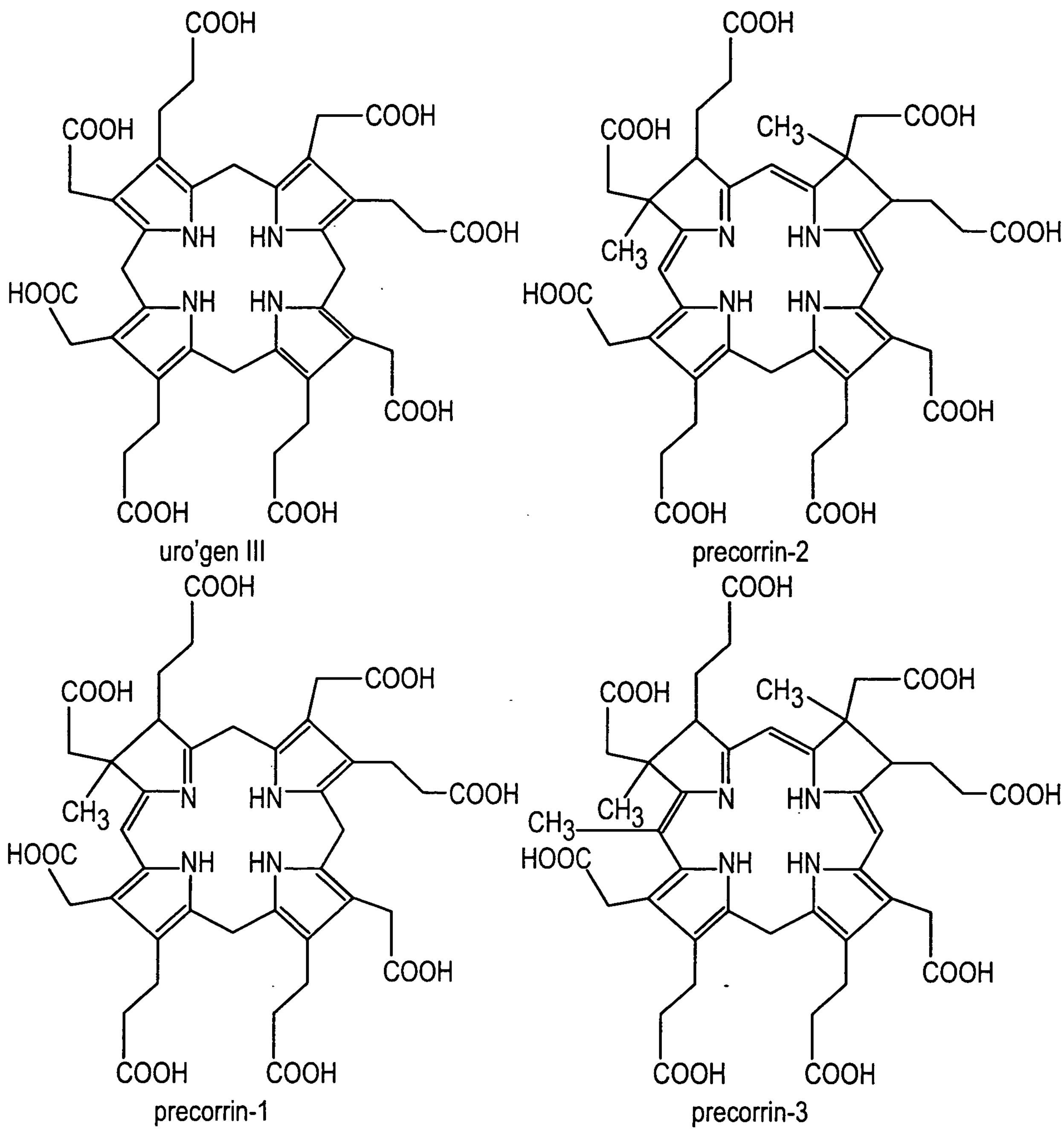
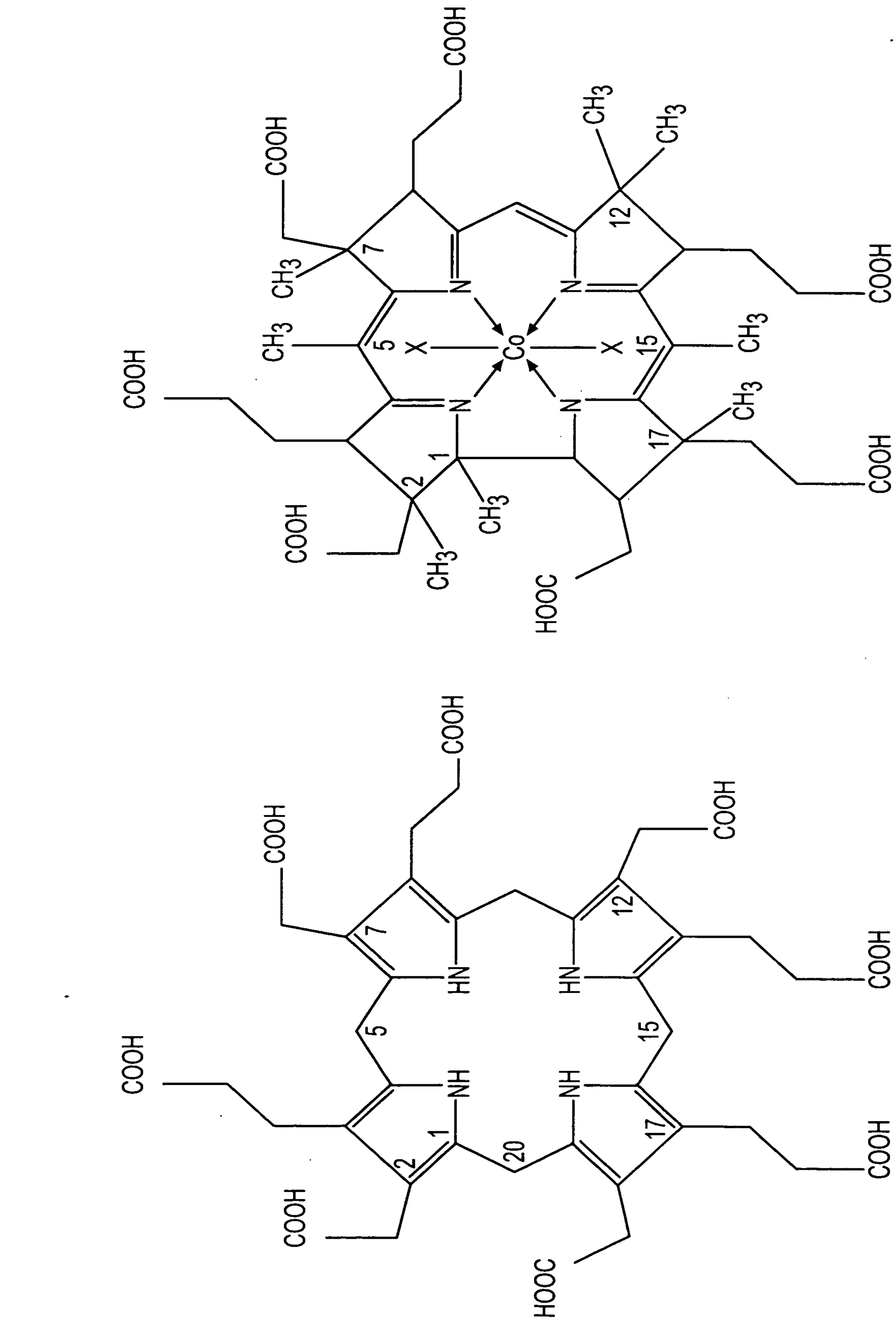


FIG. 3



URO'GEN III

COBYRINIC ACID

FIG. 4

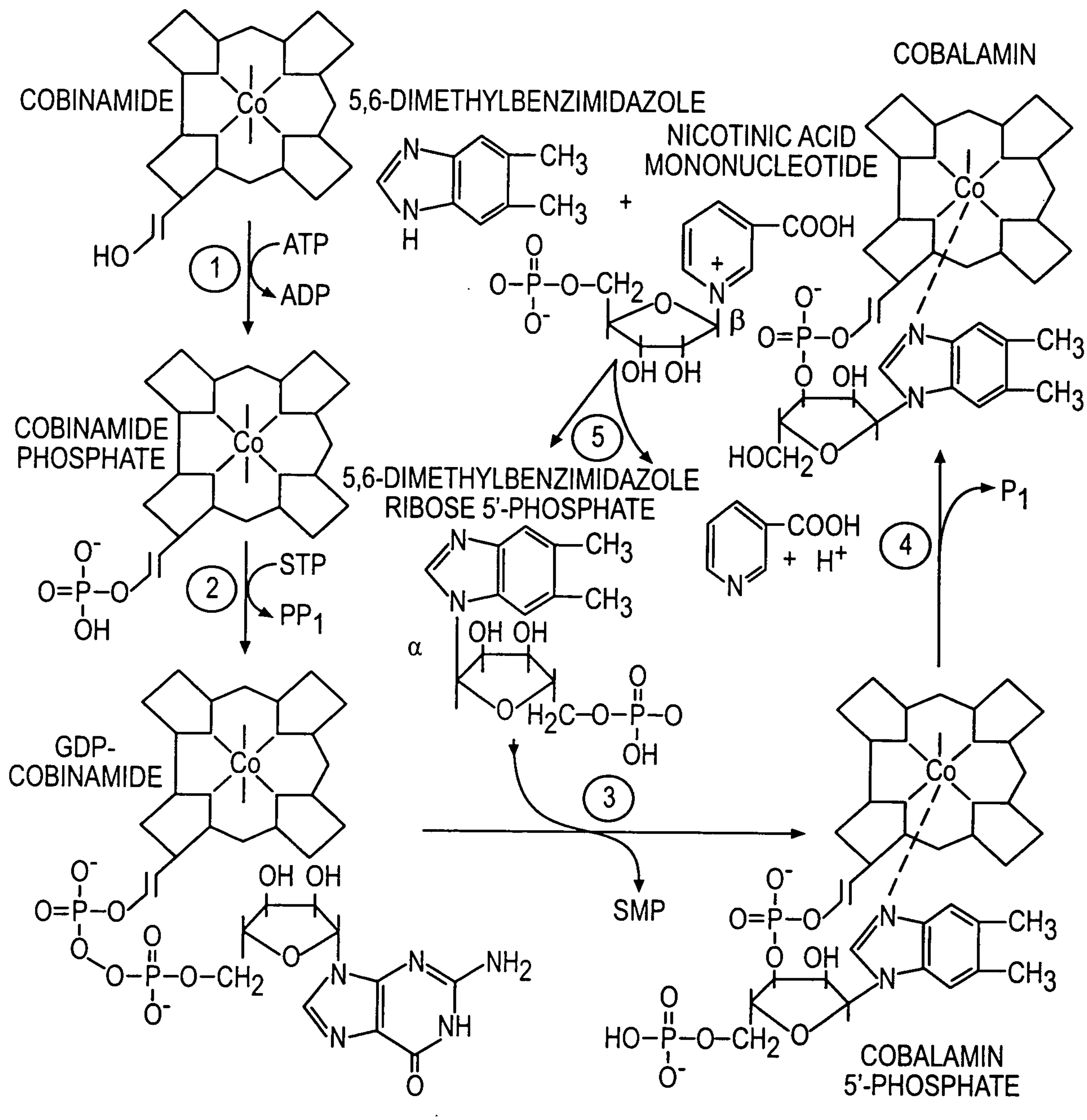

COBINAMIDE
5,6-DIMETHYLBENZIMIDAZOLE
NICOTINIC ACID MONONUCLEOTIDE
COBALAMIN
ATP
ADP
COBINAMIDE PHOSPHATE
STP
PP1
5,6-DIMETHYLBENZIMIDAZOLE RIBOSE 5'-PHOSPHATE
GDP-COBINAMIDE
SMP
P1
COBALAMIN 5'-PHOSPHATE

FIG. 5

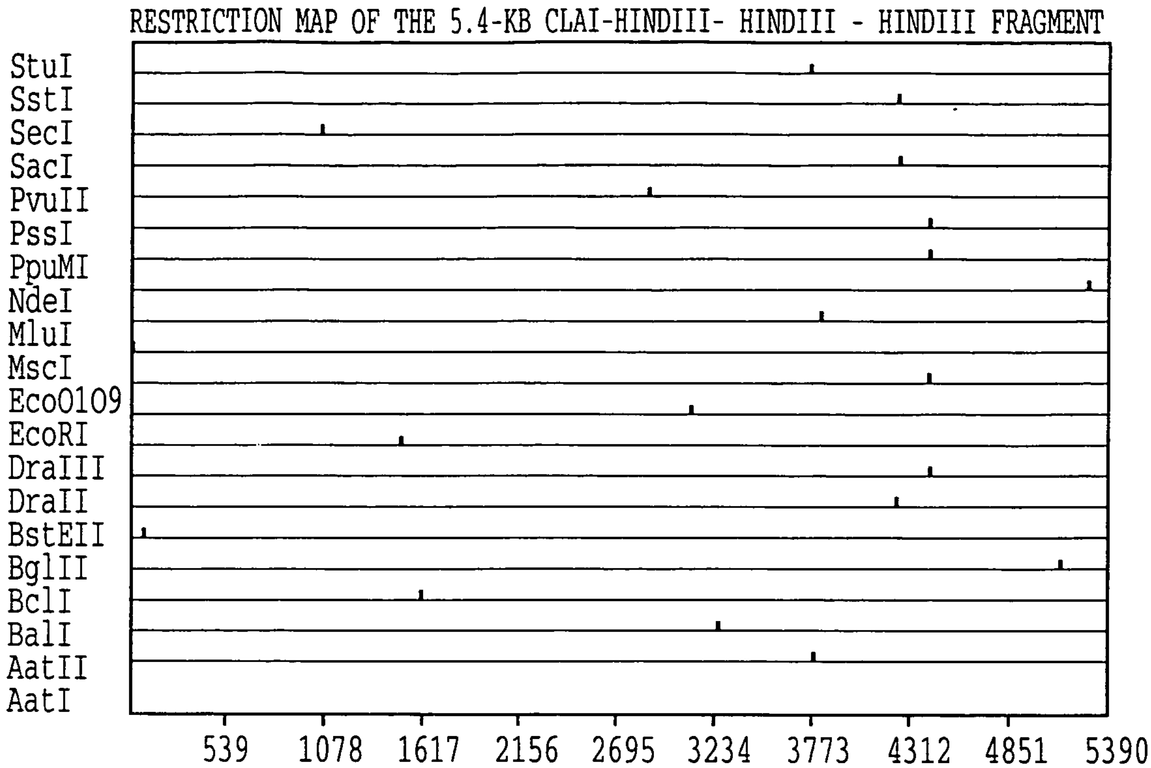

RESTRICTION MAP OF THE 5.4-KB CLAI-HINDIII- HINDIII - HINDIII FRAGMENT
StuI
SstI
SecI
SacI
PvuII
PssI
PpuMI
NdeI
MluI
MscI
Eco0109
EcoRI
DraIII
DraII
BstEII
BglII
BclI
BalI
AatII
AatI
539
1078
1617
2156
2695
3234
3773
4312
4851
5390

FIG. 6A

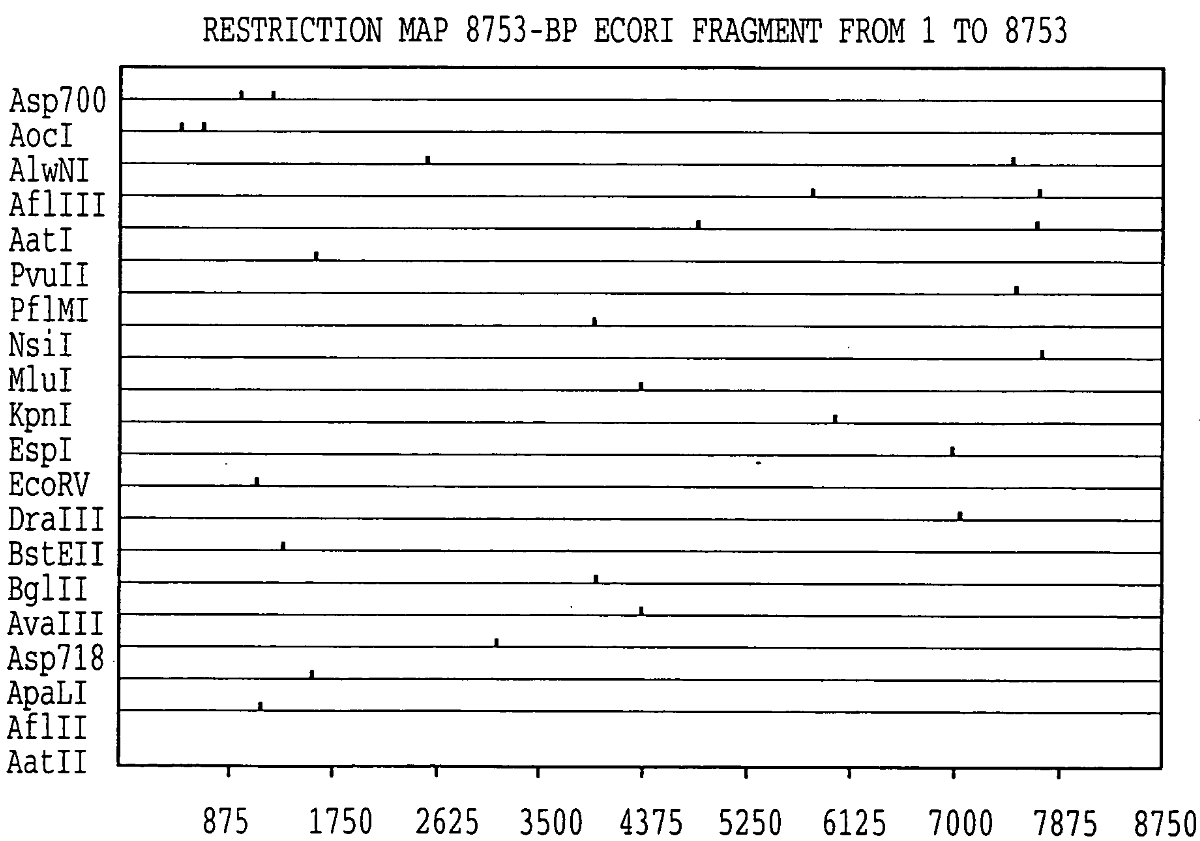

RESTRICTION MAP 8753-BP ECORI FRAGMENT FROM 1 TO 8753
Asp700
AocI
AlwNI
AflIII
AatI
PvuII
PflMI
NsiI
MluI
KpnI
EspI
EcoRV
DraIII
BstEII
BglII
AvaIII
Asp718
ApaLI
AflII
AatII
875
1750
2625
3500
4375
5250
6125
7000
7875
8750

FIG. 6B

RESTRICTION MAP OF THE 4748-BP SalI-SalI-SalI-SalI-SalI-BglI FRAGMENT

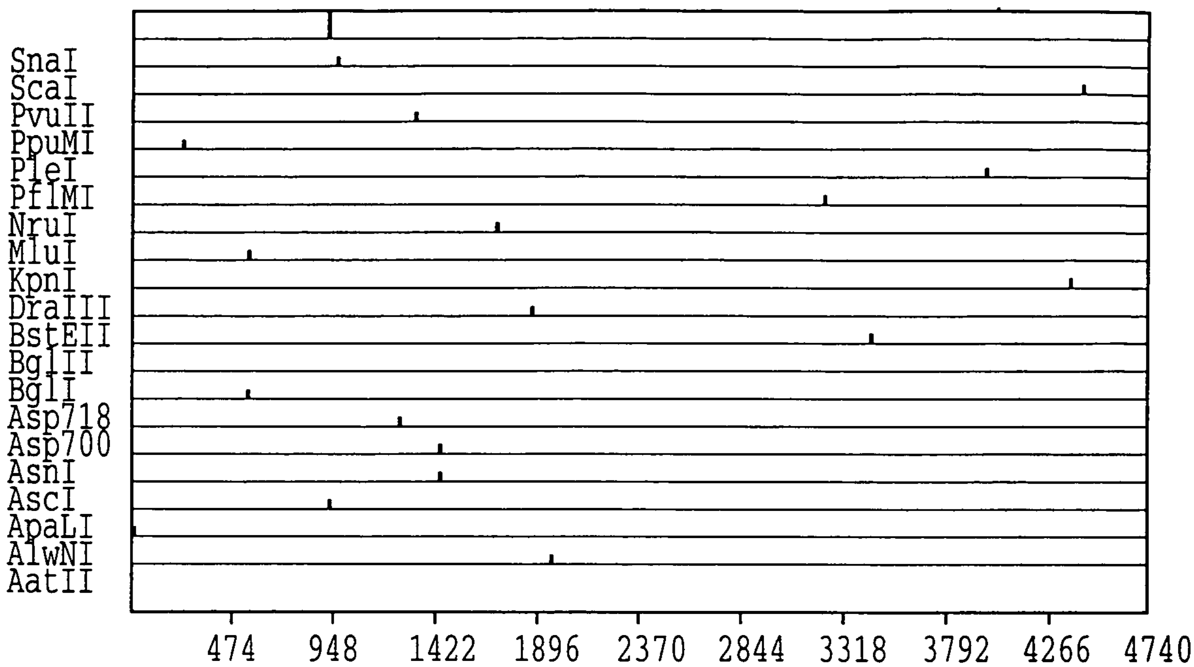


FIG. 6C

RESTRICTION MAP OF THE 3855-BP SatI-SatI-BamHI FRAGMENT

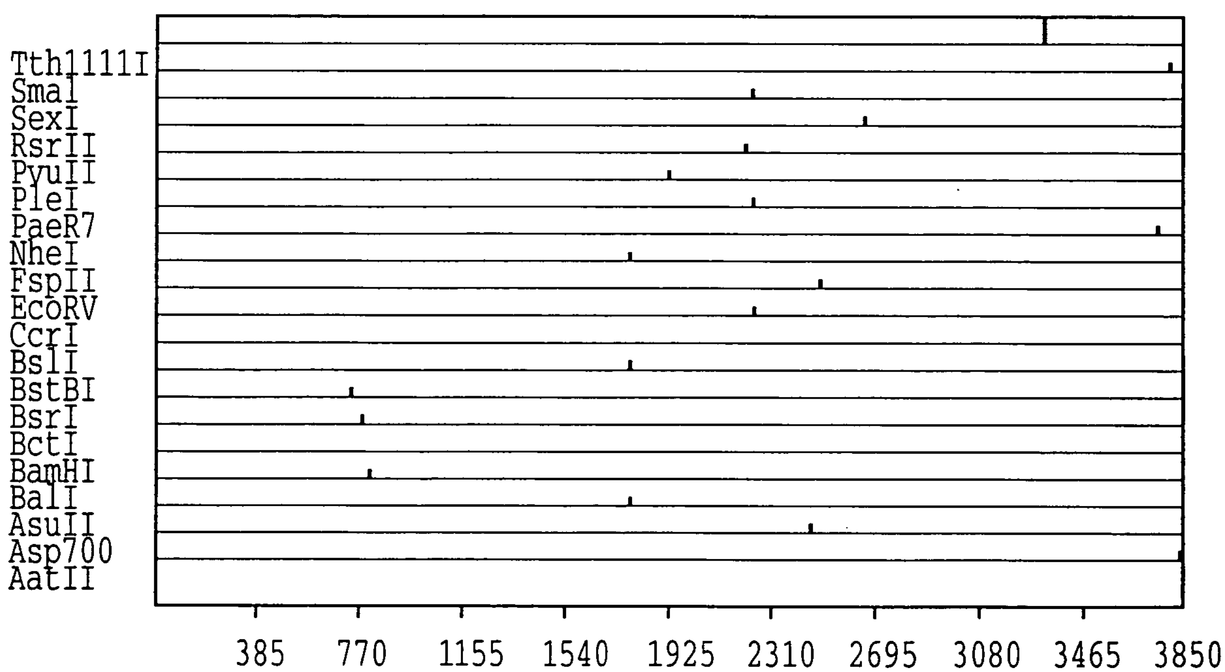


FIG. 6D

```
        10         20         30         40         50         60
GGGCTGCAGG TCGACTCTAG AATCGATGAA GCCTGCGATG AAGGCGGCGA CGAACAGGAA
CCCGACGTCC AGCTGAGATC TTAGCTACTT CGGACGCTAC TTCCGCCGCT GCTTGTCCTT

        70         80         90        100        110        120
GGCGAGCAGG TGGAAGGCGA GATCTTGCAC GGCGGGGACT CGAGAGGAGA GCTGTCAGGC
CCGCTCGTCC ACCTTCCGCT CTAGAACGTG CCGCCCCTGA GCTCTCCTCT CGACAGTCCG

       130        140        150        160        170        180
GGGATTTTCC GCCTTGTGTC AGAGCCCGGC GCGATTTGCA AAGCCTTCTG TCGCGGTGTT
CCCTAAAAGG CGGAACACAG TCTCGGGCCG CGCTAAACGT TTCGGAAGAC AGCGCCACAA

       190        200        210        220        230        240
GCTGTCCATG CAGGTGTCGA AATTGAAAAA CCGACAAAGA TTCAAAGCCT TGTTCCAGCT
CGACAGGTAC GTCCACAGCT TTAACTTTTT GGCTGTTTCT AAGTTTCGGA ACAAGGTCGA

       250        260        270        280        290        300
CGCTGTCTTT CTGGATGGAG GCGCTCTCGC CCGCATGGTG CCGAAGAAGG GCTGTCCTTG
GCGACAGAAA GACCTACCTC CGCGAGAGCG GGCGTACCAC GGCTTCTTCC CGACAGGAAC

       310        320        330        340        350        360
CGATACGGTA GGCGGATGAC GATCTTCCTC AAACGCGACA TGGCGATGGC GCAATCCGGT
GCTATGCCAT CCGCCTACTG CTAGAAGGAG TTTGCGCTGT ACCGCTACCG CGTTAGGCCA

       370        380        390        400        410        420
TTGACCGGCC TTCCGCGCTC CGGTAAAAAT GAAGGATATG CGACGGCGTC CGCTTTGGCG
AACTGGCCGG AAGGCGCGAG GCCATTTTTA CTTCCTATAC GCTGCCGCAG GCGAAACCGC

       430        440        450        460        470        480
GACTGAAAGA GCGTCCGGTG CGGCCGACCC AGTCAGGGGG GCATCAGCCG GTGCTGTCCA
CTGACTTTCT CGCAGGCCAC GCCGGCTGGG TCAGTCCCCC CGTAGTCGGC CACGACAGGT

       490        500        510        520        530        540
GATCGGCCGG GACGGATCGT CCCAGCCGGC GCTTCGTTAA GGAGAACAAC GAAGGGAGCC
CTAGCCGGCC CTGCCTAGCA GGGTCGGCCG CGAAGCAATT CCTCTTGTTG CTTCCCTCGG

       550        560        570        580        590        600
GGCCGCCGAT GCCATCGGGC CAACACTCTG CACAGACGAC GAAAGCAGGA GCCGGGCTGG
CCGGCGGCTA CGGTAGCCCG GTTGTGAGAC GTGTCTGCTG CTTTCGTCCT CGGCCCGACC
```

FIG. 7A

```
       610        620        630        640        650        660
TGCTCGGGCT CGGCTGCGAG CGTCGCACGC CGGCCGAAGA GGTGATCGCC CTTGCCGAGC
ACGAGCCCGA GCCGACGCTC GCAGCGTGCG GCCGGCTTCT CCACTAGCGG GAACGGCTCG

       670        680        690        700        710        720
GTGCGCTTGC CGATGCCGGT GTTGCGCCCG GCGATCTGCG GCTGGTCGCC TCGCTCGATG
CACGCGAACG GCTACGGCCA CAACGCGGGC CGCTAGACGC CGACCAGCGG AGCGAGCTAC

       730        740        750        760        770        780
CTCGCGCCGA GGAGCCGGCG ATCCTGGCGG CCGCTCAGCA TTTCGCGGTT CCGGCCGCGT
GAGCGCGGCT CCTCGGCCGC TAGGACCGCC GGCGAGTCGT AAAGCGCCAA GGCCGGCGCA

       790        800        810        820        830        840
TCTACGATGC CGCCACGCTC GAAGCCGAAG CTTCCCGGCT CGCCAACCCG TCCGAGATCG
AGATGCTACG GCGGTGCGAG CTTCGGCTTC GAAGGGCCGA GCGGTTGGGC AGGCTCTAGC

       850        860        870        880        890        900
TCTTTGCCTA CACGGGTTGT CATGGCGTTG CCGAGGGTGC AGCGCTCGTC GGCGCCGGTC
AGAAACGGAT GTGCCCAACA GTACCGCAAC GGCTCCCACG TCGCGAGCAG CCGCGGCCAG

       910        920        930        940        950        960
GCGAAGCCGT GCTGATTGTG CAGAAGATCG TCTCCGCCCA TGCGACGGCC GCACTTGCCG
CGCTTCGGCA CGACTAACAC GTCTTCTAGC AGAGGCGGGT ACGCTGCCGG CGTGAACGGC

       970        980        990       1000       1010       1020
GGCCGGCGAC CTTGCGCGCC GAAAAGCGCA TCCAGGCGGC GGAGGCTGTC TGATGCATTC
CCGGCCGCTG GAACGCGCGG CTTTTCGCGT AGGTCCGCCG CCTCCGACAG ACTACGTAAG

      1030       1040       1050       1060       1070       1080
TTATGTTGTT GAATTGAATC AATCTTTTGC CCGGGGTTTC TCTCAAGTGG AATCCGGTTC
AATACAACAA CTTAACTTAG TTAGAAAACG GGCCCCAAAG AGAGTTCACC TTAGGCCAAG

      1090       1100       1110       1120       1130       1140
TTTAGAGAGC GCGTCAGGCG TGCCGTTGGG TGGCGCCGAA ATACAGGTGG GACAGCACGC
AAATCTCTCG CGCAGTCCGC ACGGCAACCC ACCGCGGCTT TATGTCCACC CTGTCGTGCG

      1150       1160       1170       1180       1190       1200
ATGATCGACG ACCTCTTTGC CGGATTGCCG GCGCTCGAAA AAGGTTCGGT CTGGCTGGTC
TACTAGCTGC TGGAGAAACG GCCTAACGGC CGCGAGCTTT TTCCAAGCCA GACCGACCAG
```

FIG. 7B

```
      1210       1220       1230       1240       1250       1260
GGCGCCGGCC CCGGCGATCC CGGCCTGTTG ACGCTGCATG CGGCCAATGC GCTGCGCCAG
CCGCGGCCGG GGCCGCTAGG GCCGGACAAC TGCGACGTAC GCCGGTTACG CGACGCGGTC

      1270       1280       1290       1300       1310       1320
GCGGATGTGA TCGTGCATGA TGCGCTGGTC AACGAGGATT GCCTGAAGCT CGCGCGGCCG
CGCCTACACT AGCACGTACT ACGCGACCAG TTGCTCCTAA CGGACTTCGA GCGCGCCGGC

      1330       1340       1350       1360       1370       1380
GGCGCCGTGC TGGAGTTTGC GGGCAAGCGT GGCGGCAAGC CGTCGCCGAA GCAGCGCGAC
CCGCGGCACG ACCTCAAACG CCCGTTCGCA CCGCCGTTCG GCAGCGGCTT CGTCGCGCTG

      1390       1400       1410       1420       1430       1440
ATCTCGCTTC GCCTCGTCGA ACTCGCGCGC GCCGGCAACC GGGTGCTGCG CCTCAAAGGC
TAGAGCGAAG CGGAGCAGCT TGAGCGCGCG CGGCCGTTGG CCCACGACGC GGAGTTTCCG

      1450       1460       1470       1480       1490       1500
GGCGATCCCT TCGTCTTCGG TCGCGGTGGC GAGGAGGCGC TGACGCTGGT CGAACACCAG
CCGCTAGGGA AGCAGAAGCC AGCGCCACCG CTCCTCCGCG ACTGCGACCA GCTTGTGGTC

      1510       1520       1530       1540       1550       1560
GTGCCGTTCC GAATCGTGCC CGGCATCACC GCCGGTATCG GCGGGCTTGC CTATGCCGGC
CACGGCAAGG CTTAGCACGG GCCGTAGTGG CGGCCATAGC CGCCCGAACG GATACGGCCG

      1570       1580       1590       1600       1610       1620
ATTCCCGTGA CCCATCGCGA GGTCAACCAC GCGGTCACTT TCCTGACTGG CCATGATTCC
TAAGGGCACT GGGTAGCGCT CCAGTTGGTG CGCCAGTGAA AGGACTGACC GGTACTAAGG

      1630       1640       1650       1660       1670       1680
TCCGGCCTGG TGCCGGATCG CATCAACTGG CAGGGCATCG CCAGCGGCTC GCCTGTCATC
AGGCCGGACC ACGGCCTAGC GTAGTTGACC GTCCCGTAGC GGTCGCCGAG CGGACAGTAG

      1690       1700       1710       1720       1730       1740
GTCATGTACA TGGCGATGAA ACATATCGGC GCGATCACCG CCAACCTCAT TGCCGGCGGC
CAGTACATGT ACCGCTACTT TGTATAGCCG CGCTAGTGGC GGTTGGAGTA ACGGCCGCCG

      1750       1760       1770       1780       1790       1800
CGCTCGCCGG ACGAACCGGT CGCCTTCGTC TGCAACGCCG CGACGCCGCA GCAGGCGGTG
GCGAGCGGCC TGCTTGGCCA GCGGAAGCAG ACGTTGCGGC GCTGCGGCGT CGTCCGCCAC
```

FIG. 7C

```
      1810       1820       1830       1840       1850       1860
CTGGAAACGA CGCTTGCGCG TGCAGAGGCC GATGTTGCGG CGGCAGGGCT GGAGCCGCCG
GACCTTTGCT GCGAACGCGC ACGTCTCCGG CTACAACGCC GCCGTCCCGA CCTCGGCGGC

      1870       1880       1890       1900       1910       1920
GCGATCGTCG TCGTCGGCGA GGTGGTGCGG CTGCGCGCAG CGCTCGACTG GATCGGCGCG
CGCTAGCAGC AGCAGCCGCT CCACCACGCC GACGCGCGTC GCGAGCTGAC CTAGCCGCGC

      1930       1940       1950       1960       1970       1980
CTGGACGGGC GCAAGCTTGC CGCCGACCCG TTCGCCAATC GCATTCTCAG GAACCCGGCA
GACCTGCCCG CGTTCGAACG GCGGCTGGGC AAGCGGTTAG CGTAAGAGTC CTTGGGCCGT

      1990       2000       2010       2020       2030       2040
TGAGCGGATT GCTGATTGCC GCACCCGCGT CCGGCTCCGG CAAGACGACG GTGACGCTCG
ACTCGCCTAA CGACTAACGG CGTGGGCGCA GGCCGAGGCC GTTCTGCTGC CACTGCGAGC

      2050       2060       2070       2080       2090       2100
GGCTGATGCG CGCCCTGAAG AGGCGCGGCG TGGCGATCGC GCCCGGCAAG GCGGGGCCGG
CCGACTACGC GCGGGACTTC TCCGCGCCGC ACCGCTAGCG CGGGCCGTTC CGCCCCGGCC

      2110       2120       2130       2140       2150       2160
ACTATATCGA TCCCGCTTTC CACGCGGCAG CGACCGGCGA GCCCTGCTTC AACTACGACC
TGATATAGCT AGGGCGAAAG GTGCGCCGTC GCTGGCCGCT CGGGACGAAG TTGATGCTGG

      2170       2180       2190       2200       2210       2220
CCTGGGCGAT GCGCCCGGAA CTGCTGCTTG CCAATGCGTC GCATGTGGCC TCCGGCGGGC
GGACCCGCTA CGCGGGCCTT GACGACGAAC GGTTACGCAG CGTACACCGG AGGCCGCCCG

      2230       2240       2250       2260       2270       2280
GCACATTGAT CGTCGAGGCG ATGATGGGAC TGCATGACGG TGCTGCCGAC GGCTCGGGAA
CGTGTAACTA GCAGCTCCGC TACTACCCTG ACGTACTGCC ACGACGGCTG CCGAGCCCTT

      2290       2300       2310       2320       2330       2340
CGCCAGCGGA CCTCGCCGCG ACGCTGAACC TTGCGGTCAT TCTGGTGGTC GATTGCGCCC
GCGGTCGCCT GGAGCGGCGC TGCGACTTGG AACGCCAGTA AGACCACCAG CTAACGCGGG

      2350       2360       2370       2380       2390       2400
GCATGTCCCA GTCGGTTGCC GCCCTCGTGC GCGGCTATGC GGATCATCGC GACGATATCC
CGTACAGGGT CAGCCAACGG CGGGAGCACG CGCCGATACG CCTAGTAGCG CTGCTATAGG
```

FIG. 7D

```
      2410       2420       2430       2440       2450       2460
GGGTGGTTGG CGTCATCCTC AACAAGGTCG GCAGCGATCG GCATGAAATG ATGCTGCGCG
CCCACCAACC GCAGTAGGAG TTGTTCCAGC CGTCGCTAGC CGTACTTTAC TACGACGCGC

      2470       2480       2490       2500       2510       2520
ATGCGCTCGG CAAGGTGCGC ATGCCTGTCT TCGGCGTGCT CCGGCAGGAC AGCGCATTGC
TACGCGAGCC GTTCCACGCG TACGGACAGA AGCCGCACGA GGCCGTCCTG TCGCGTAACG

      2530       2540       2550       2560       2570       2580
AACTGCCGGA GCGCCATCTC GGGCTCGTGC AGGCGGGCGA ACACTCAGCG CTTGAGGGCT
TTGACGGCCT CGCGGTAGAG CCCGAGCACG TCCGCCCGCT TGTGAGTCGC GAACTCCCGA

      2590       2600       2610       2620       2630       2640
TCATCGAGGC GGCGGCCGCG CGGGTCGAGG CTGCCTGCGA TCTCGACGCC ATCCGCCTGA
AGTAGCTCCG CCGCCGGCGC GCCCAGCTCC GACGGACGCT AGAGCTGCGG TAGGCGGACT

      2650       2660       2670       2680       2690       2700
TCGCGACGAT TTTCCCGCAG GTGCCCGCGG CGGCCGATGC CGAGCGTTTG CGGCCGCTCG
AGCGCTGCTA AAAGGGCGTC CACGGGCGCC GCCGGCTACG GCTCGCAAAC GCCGGCGAGC

      2710       2720       2730       2740       2750       2760
GTCAGCGCAT CGCGGTCGCG CGCGATATCG CCTTTGCCTT CTGCTACGAG CACCTGCTTT
CAGTCGCGTA GCGCCAGCGC GCGCTATAGC GGAAACGGAA GACGATGCTC GTGGACGAAA

      2770       2780       2790       2800       2810       2820
ACGGCTGGCG GCAAGGCGGC GCGGAGATTT CCTTCTTCTC GCCGCTCGCC GACGAGGGGC
TGCCGACCGC CGTTCCGCCG CGCCTCTAAA GGAAGAAGAG CGGCGAGCGG CTGCTCCCCG

      2830       2840       2850       2860       2870       2880
CGGATGCGGC AGCCGATGCC GTCTATCTTC CGGGGGGTTA TCCGGAGCTG CATGCGGGGC
GCCTACGCCG TCGGCTACGG CAGATAGAAG GCCCCCCAAT AGGCCTCGAC GTACGCCCCG

      2890       2900       2910       2920       2930       2940
AGCTGAGCGC CGCCGCCCGA TTCCGTTCCG GCATGCATTC CGCGGCGGAA CGCGGCGCCC
TCGACTCGCG GCGGCGGGCT AAGGCAAGGC CGTACGTAAG GCGCCGCCTT GCGCCGCGGG

      2950       2960       2970       2980       2990       3000
GCATCTTCGG CGAGTGCGGC GGCTATATGG TGCTCGGCGA AGGGCTTGTC GCTGCCGATG
CGTAGAAGCC GCTCACGCCG CCGATATACC ACGAGCCGCT TCCCGAACAG CGACGGCTAC
```

FIG. 7E

```
      3010       3020       3030       3040       3050       3060
GCACACGCTA CGACATGCTC GGCCTGCTGC CGCTCGTAAC CAGTTTTGCC GAGCGCAGGC
CGTGTGCGAT GCTGTACGAG CCGGACGACG GCGAGCATTG GTCAAAACGG CTCGCGTCCG

      3070       3080       3090       3100       3110       3120
GGCACCTCGG CTATCGCCGC GTCGTGCCTG TCGACAACGC CTTCTTCGAT GGACCCATGA
CCGTGGAGCC GATAGCGGCG CAGCACGGAC AGCTGTTGCG GAAGAAGCTA CCTGGGTACT

      3130       3140       3150       3160       3170       3180
CGGCGCACGA ATTCCACTAT GCGACCATCG TCGCCGAAGG GGCGGCCGAT CGGCTGTTTG
GCCGCGTGCT TAAGGTGATA CGCTGGTAGC AGCGGCTTCC CCGCCGGCTA GCCGACAAAC

      3190       3200       3210       3220       3230       3240
CGGTCAGCGA CGCCGCCGGC GAGGATCTCG GCCAGGCGGG CCTCCGGCGC GGCCCTGTCG
GCCAGTCGCT GCGGCGGCCG CTCCTAGAGC CGGTCCGCCC GGAGGCCGCG CCGGGACAGC

      3250       3260       3270       3280       3290       3300
CCGGTTCCTT CATGCATCTG ATCGACGTCG CAGGTGCTGC ATGAGCGCAC CGATCGTTCA
GGCCAAGGAA GTACGTAGAC TAGCTGCAGC GTCCACGACG TACTCGCGTG GCTAGCAAGT

      3310       3320       3330       3340       3350       3360
TGGTGGCGGC ATCACCGAGG CCGCAGCGCG CTATGGCGGC CGGCCTGAAG ACTGGCTCGA
ACCACCGCCG TAGTGGCTCC GGCGTCGCGC GATACCGCCG GCCGGACTTC TGACCGAGCT

      3370       3380       3390       3400       3410       3420
TCTGTCGACC GGCATCAATC CATGCCCCGT CGCCTTGCCC GCGGTCCCTG AGCGCGCCTG
AGACAGCTGG CCGTAGTTAG GTACGGGGCA GCGGAACGGG CGCCAGGGAC TCGCGCGGAC

      3430       3440       3450       3460       3470       3480
GCACCGGCTG CCGGATCGGC AGACGGTAGA TGATGCGCGG AGCGCCGCCG CCGACTACTA
CGTGGCCGAC GGCCTAGCCG TCTGCCATCT ACTACGCGCC TCGCGGCGGC GGCTGATGAT

      3490       3500       3510       3520       3530       3540
CCGCACCAAC GGCGTGCTGC CTTTGCCGGT GCCGGGCACC CAGTCGGTGA TCCAGCTCCT
GGCGTGGTTG CCGCACGACG GAAACGGCCA CGGCCCGTGG GTCAGCCACT AGGTCGAGGA

      3550       3560       3570       3580       3590       3600
GCCACGTCTT GCTCCGGCCA ACAGGCACGT CGCGATTTTC GGGCCGACCT ATGGCGAGTA
CGGTGCAGAA CGAGGCCGGT TGTCCGTGCA GCGCTAAAAG CCCGGCTGGA TACCGCTCAT
```

FIG. 7F

```
      3610       3620       3630       3640       3650       3660
TGCCCGCGTG CTTGAAGCGG CCGGCTTTGC TGTCGATCGC GTCGCGGATG CCGACGCGCT
ACGGGCGCAC GAACTTCGCC GGCCGAAACG ACAGCTAGCG CAGCGCCTAC GGCTGCGCGA

      3670       3680       3690       3700       3710       3720
CACGGCCGAA CATGGGCTTG TCATCGTCGT CAACCCCAAC AACCCGACCG GCCGCGCCTT
GTGCCGGCTT GTACCCGAAC AGTAGCAGCA GTTGGGGTTG TTGGGCTGGC CGGCGCGGAA

      3730       3740       3750       3760       3770       3780
GGCGCCGGCG GAGCTTCTGG CGATCGCCGC AAGGCAGAAG GCGAGCGGCG GACTGCTGCT
CCGCGGCCGC CTCGAAGACC GCTAGCGGCG TTCCGTCTTC CGCTCGCCGC CTGACGACGA

      3790       3800       3810       3820       3830       3840
GGTCGATGAG GCCTTCGGCG ATCTTGAGCC GCAACTGAGT GTCGCTGGTC ACGCGTCAGG
CCAGCTACTC CGGAAGCCGC TAGAACTCGG CGTTGACTCA CAGCGACCAG TGCGCAGTCC

      3850       3860       3870       3880       3890       3900
GCAAGGCAAC CTCATCGTCT TCCGCTCCTT CGGCAAGTTC TTCGGCCTTG CGGGCCTGCG
CGTTCCGTTG GAGTAGCAGA AGGCGAGGAA GCCGTTCAAG AAGCCGGAAC GCCCGGACGC

      3910       3920       3930       3940       3950       3960
CCTCGGCTTC GTCGTTGCGA CCGAGCCAGT GCTTGCATCC TTTGCCGATT GGCTCGGTCC
GGAGCCGAAG CAGCAACGCT GGCTCGGTCA CGAACGTAGG AAACGGCTAA CCGAGCCAGG

      3970       3980       3990       4000       4010       4020
CTGGGCTGTC TCCGGCCCGG CGTTGACGAT CTCGAAAGCG CTGATGCAGG GCGATACGAA
GACCCGACAG AGGCCGGGCC GCAACTGCTA GAGCTTTCGC GACTACGTCC CGCTATGCTT

      4030       4040       4050       4060       4070       4080
GGCGATCGCG GCGGGCATCC TCGAGCGTCG CGCCGGCCTC GATGCGGCTC TCGATGGGGC
CCGCTAGCGC CGCCCGTAGG AGCTCGCAGC GCGGCCGGAG CTACGCCGAG AGCTACCCCG

      4090       4100       4110       4120       4130       4140
AGGGCTCAAC CGTATCGGCG GCACGGGGCT ATTCGTGCTG GTCGAGCATC CCAGGGCAGC
TCCCGAGTTG GCATAGCCGC CGTGCCCCGA TAAGCACGAC CAGCTCGTAG GGTCCCGTCG

      4150       4160       4170       4180       4190       4200
TCTGCTGCAG GAGCGGCTCT GCGAGGCCCA TATTCTCACG CGCAAGTTCG ACTATGCCCC
AGACGACGTC CTCGCCGAGA CGCTCCGGGT ATAAGAGTGC GCGTTCAAGC TGATACGGGG
```

FIG. 7G

```
      4210       4220       4230       4240       4250       4260
GACCTGGCTC AGGGTCGGTC TTGCGCCTGA CGCGGCTGGT GACCGACGGC TGGCGGACGC
CTGGACCGAG TCCCAGCCAG AACGCGGACT GCGCCGACCA CTGGCTGCCG ACCGCCTGCG

      4270       4280       4290       4300       4310       4320
GCTTGCCCGC ATGGAGCTCT GAGGTGTCGG AGACGATCCT GCTCATTCTC GCGCTGGCGC
CGAACGGGCG TACCTCGAGA CTCCACAGCC TCTGCTAGGA CGAGTAAGAG CGCGACCGCG

      4330       4340       4350       4360       4370       4380
TGGTGATCGA CCGCGTTGTC GGCGATCCGG ACTGGCTCTG GGCGCGCGTG CCGCATCCGG
ACCACTAGCT GGCGCAACAG CCGCTAGGCC TGACCGAGAC CCGCGCGCAC GGCGTAGGCC

      4390       4400       4410       4420       4430       4440
TCGTGTTTTT CGGCAAGGCC ATCGGCTTTT TCGACGCGCG GCTGAACCGG GAGGACCTCG
AGCACAAAAA GCCGTTCCGG TAGCCGAAAA AGCTGCGCGC CGACTTGGCC CTCCTGGAGC

      4450       4460       4470       4480       4490       4500
AGGATAGCGC GCGCAAATTT CGTGGCGTCG TCGCGATCCT TTTGTTGCTT GGCATCAGCG
TCCTATCGCG CGCGTTTAAA GCACCGCAGC AGCGCTAGGA AAACAACGAA CCGTAGTCGC

      4510       4520       4530       4540       4550       4560
CCTGGTTCGG CCATCTGCTG CATCGCCTGT TCGCCGTCCT CGGACCGCTC GGCTTTCTGC
GGACCAAGCC GGTAGACGAC GTAGCGGACA AGCGGCAGGA GCCTGGCGAG CCGAAAGACG

      4570       4580       4590       4600       4610       4620
TCGAGGCGGT TCTGGTCGCG GTCTTCCTGG CACAGAAGAG CCTCGCCGAT CACGTGCGTC
AGCTCCGCCA AGACCAGCGC CAGAAGGACC GTGTCTTCTC GGAGCGGCTA GTGCACGCAG

      4630       4640       4650       4660       4670       4680
GCGTGGCCGG GGGCTTGCGA CAGGGCGGGC TGGAAGGCGG GCGTGCCGCC GTGTCGATGA
CGCACCGGCC CCCGAACGCT GTCCCGCCCG ACCTTCCGCC CGCACGGCGG CACAGCTACT

      4690       4700       4710       4720       4730       4740
TCGTTGGTCG CGATCCAAAG ACGCTCGACG AGCCGGCGGT CTGCCGTGCC GCGATCGAAA
AGCAACCAGC GCTAGGTTTC TGCGAGCTGC TCGGCCGCCA GACGGCACGG CGCTAGCTTT

      4750       4760       4770       4780       4790       4800
GCCTTGCCGA GAATTTCTCC GACGGCGTCG TGGCGCCGGC CTTCTGGTAC GCGGTTGCCG
CGGAACGGCT CTTAAAGAGG CTGCCGCAGC ACCGCGGCCG GAAGACCATG CGCCAACGGC
```

FIG. 7H

```
      4810       4820       4830       4840       4850       4860
GCCTGCCGGG GCTTCTTGCC TACAAGATGC TGAACACCGC CGATTCGATG ATCGGCCACA
CGGACGGCCC CGAAGAACGG ATGTTCTACG ACTTGTGGCG GCTAAGCTAC TAGCCGGTGT

      4870       4880       4890       4900       4910       4920
AGTCGCCGAA ATATCTGCAC TTCGGCTGGG CCTCGGCCCG ACTCGACGAT CTCGCCAACC
TCAGCGGCTT TATAGACGTG AAGCCGACCC GGAGCCGGGC TGAGCTGCTA GAGCGGTTGG

      4930       4940       4950       4960       4970       4980
TGCCGGCAGC GAGGCTCTCG ATCCTTTTGA TCTCAGCCGG TGCGCTGATC CATCGTGGCG
ACGGCCGTCG CTCCGAGAGC TAGGAAAACT AGAGTCGGCC ACGCGACTAG GTAGCACCGC

      4990       5000       5010       5020       5030       5040
CCAGCGCCGC CAAGGATGCG CTGACCGTGG CCCTTCGCGA CCATGGCCTG CACCGCTCGC
GGTCGCGGCG GTTCCTACGC GACTGGCACC GGGAAGCGCT GGTACCGGAC GTGGCGAGCG

      5050       5060       5070       5080       5090       5100
CGAACTCCGG CTGGCCGGAA GCGGCCATGG CCGGCGCGCT CGATCTGCAG CTTGCCGGTC
GCTTGAGGCC GACCGGCCTT CGCCGGTACC GGCCGCGCGA GCTAGACGTC GAACGGCCAG

      5110       5120       5130       5140       5150       5160
CGCGGATCTA TGGCGGCGTC AAGGTCAGCG AACCTATGAT CAACGGTCCG GGCCGAGCGG
GCGCCTAGAT ACCGCCGCAG TTCCAGTCGC TTGGATACTA GTTGCCAGGC CCGGCTCGCC

      5170       5180       5190       5200       5210       5220
TTGCAACAAG CGAAGACATC GACGCCGGTA TTGCTGTATT TTATGGCGCC TGTACGGTCA
AACGTTGTTC GCTTCTGTAG CTGCGGCCAT AACGACATAA AATACCGCGG ACATGCCAGT

      5230       5240       5250       5260       5270       5280
TGGCCGGGTT TGTTCTTGCA ATCGCAATGA TTTGATCGCG GAAGTTGACC TTCGCATTAA
ACCGGCCCAA ACAAGAACGT TAGCGTTACT AAACTAGCGC CTTCAACTGG AAGCGTAATT

      5290       5300       5310       5320       5330       5340
GACTCTGCTT TCCATATGTA TTAAGATCGT ATCATATTCG ATCAGTTATT CTCCTGGAAC
CTGAGACGAA AGGTATACAT AATTCTAGCA TAGTATAAGC TAGTCAATAA GAGGACCTTG

      5350       5360       5370       5380       5390       5400
GTTTGGTTCC ACCGGTACGT GTTCGTCTTC CCGGAGAGAG AAGCATGCGC AAAAGCTT
CAAACCAAGG TGGCCATGCA CAAGCAGAAG GGCCTCTCTC TTCGTACGCG TTTTCGAA
```

FIG. 7I

10	20	30	40	50	60
GAATTCGCCA	GCGCCTACAT	GGCTGACCTC	AAGCAGTTCC	TCGTGGCCCA	GAAGAACGAG
CTTAAGCGGT	CGCGGATGTA	CCGACTGGAG	TTCGTCAAGG	AGCACCGGGT	CTTCTTGCTC

70	80	90	100	110	120
GGCCGGCAGA	TTTTCCCTCG	CGGGCCTGAG	TATTTTCGCG	CGCTCGACCT	GACGCCGCTC
CCGGCCGTCT	AAAAGGGAGC	GCCCGGACTC	ATAAAAGCGC	GCGAGCTGGA	CTGCGGCGAG

130	140	150	160	170	180
GACAAGGTGC	GCGTGGTCAT	TCTCGGCCAG	GATCCCTATC	ACGGTGACGG	CCAGGCGCAT
CTGTTCCACG	CGCACCAGTA	AGAGCCGGTC	CTAGGGATAG	TGCCACTGCC	GGTCCGCGTA

190	200	210	220	230	240
GGGCTCTGCT	TCAGCGTTCG	CCCCGGTGTC	CGGACGCCGC	CGTCGCTGGT	CAACATCTAC
CCCGAGACGA	AGTCGCAAGC	GGGGCCACAG	GCCTGCGGCG	GCAGCGACCA	GTTGTAGATG

250	260	270	280	290	300
AAGGAACTGA	ATACCGATCT	CGGTATTCCG	CCGGCGCGTC	ACGGTTTTCT	CGAAAGCTGG
TTCCTTGACT	TATGGCTAGA	GCCATAAGGC	GGCCGCGCAG	TGCCAAAAGA	GCTTTCGACC

310	320	330	340	350	360
GCAAGGCAGG	GCGTGCTGCT	TTTGAACAGC	GTGCTGACGG	TAGAGCGCGG	GAACGTGCGT
CGTTCCGTCC	CGCACGACGA	AAACTTGTCG	CACGACTGCC	ATCTCGCGCC	CTTGCACGCA

370	380	390	400	410	420
CACACCAGGG	TCACGGTTGG	GAAAAGTTCA	CGGATGCGAT	CATCCGTGCG	GTCAACGAGG
GTGTGGTCCC	AGTGCCAACC	CTTTTCAAGT	GCCTACGCTA	GTAGGCACGC	CAGTTGCTCC

430	440	450	460	470	480
CCGAGCATCC	CGTCGTCTTC	ATGCTTTGGG	GCTCCTATGC	GCAGAAGAAG	GCGGCCTTCG
GGCTCGTAGG	GCAGCAGAAG	TACGAAACCC	CGAGGATACG	CGTCTTCTTC	CGCCGGAAGC

490	500	510	520	530	540
TCGACCGCTC	GCGCCATCTT	GTCCTGAGGG	CACCACATCC	GTCGCCGCTC	TCAGCCCATT
AGCTGGCGAG	CGCGGTAGAA	CAGGACTCCC	GTGGTGTAGG	CAGCGGCGAG	AGTCGGGTAA

550	560	570	580	590	600
CCGGCTTTCT	CGGCTGCCGG	CATTTTTCCC	AGGCCAATGC	CTTCCTCGAA	AGCAAAGGCT
GGCCGAAAGA	GCCGACGGCC	GTAAAAAGGG	TCCGGTTACG	GAAGGAGCTT	TCGTTTCCGA

FIG. 8A

```
       610        620        630        640        650        660
TCGATCCGAT CGACTGGCGG CTGCCGGAAA ATCCGGCTGC GGACATCAAC TGAAGGCTTG
AGCTAGGCTA GCTGACCGCC GACGGCCTTT TAGGCCGACG CCTGTAGTTG ACTTCCGAAC

       670        680        690        700        710        720
GCGCGAATGA CGGCTTTGTC GTCGCCCTGA GGTCTTGCCT TGGCGGCGGC GATCCGCCTA
CGCGCTTACT GCCGAAACAG CAGCGGGACT CCAGAACGGA ACCGCCGCCG CTAGGCGGAT

       730        740        750        760        770        780
AGACGCCCGA ACGAAATGGC GGAGGCGGGC ATGCGCAAAA TTCTGATCAT CGGCATCGGT
TCTGCGGGCT TGCTTTACCG CCTCCGCCCG TACGCGTTTT AAGACTAGTA GCCGTAGCCA

       790        800        810        820        830        840
TCGGGCAATC CCGAACACAT GACCGTGCAG GCGATCAACG CGCTGAACTG CGCCGACGTG
AGCCCGTTAG GGCTTGTGTA CTGGCACGTC CGCTAGTTGC GCGACTTGAC GCGGCTGCAC

       850        860        870        880        890        900
CTCTTTATCC CGACCAAGGG AGCGAAGAAG ACCGAGCTTG CCGAAGTGCG CCGCGACATC
GAGAAATAGG GCTGGTTCCC TCGCTTCTTC TGGCTCGAAC GGCTTCACGC GGCGCTGTAG

       910        920        930        940        950        960
TGCGCCCGCT ACGTCACGCG CAAGGACAGC CGCACCGTCG AGTTCGCGGT GCCCGTGCGG
ACGCGGGCGA TGCAGTGCGC GTTCCTGTCG GCGTGGCAGC TCAAGCGCCA CGGGCACGCC

       970        980        990       1000       1010       1020
CGCACCGAAG GCGTCAGCTA TGACGGCAGC GTCGATGACT GGCACGCCCA GATCGCTGGG
GCGTGGCTTC CGCAGTCGAT ACTGCCGTCG CAGCTACTGA CCGTGCGGGT CTAGCGACCC

      1030       1040       1050       1060       1070       1080
ATTTACGAAG CGCTTCTATC GAAGGAGTTG GGCGAAGAGG GAACTGGCGC GTTTCTCGTC
TAAATGCTTC GCGAAGATAG CTTCCTCAAC CCGCTTCTCC CTTGACCGCG CAAAGAGCAG

      1090       1100       1110       1120       1130       1140
TGGGGCGACC CGATGCTCTA TGACAGCACC ATTCGCATCG TCGAGCGGGT CAAGGCACGC
ACCCCGCTGG GCTACGAGAT ACTGTCGTGG TAAGCGTAGC AGCTCGCCCA GTTCCGTGCG

      1150       1160       1170       1180       1190       1200
GGTGAGGTCG CCTTCGCCTA CGACGTCATT CCCGGGATCA CCAGTCTGCA GGCGCTTTGC
CCACTCCAGC GGAAGCGGAT GCTGCAGTAA GGGCCCTAGT GGTCAGACGT CCGCGAAACG
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FIG. 8B

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       1210       1220       1230       1240       1250       1260
GCCAGCCACC GCATTCCGCT GAACCTCGTC GGCAAGCCGG TGGAGATCAC CACGGGGCGT
CGGTCGGTGG CGTAAGGCGA CTTGGAGCAG CCGTTCGGCC ACCTCTAGTG GTGCCCCGCA

       1270       1280       1290       1300       1310       1320
CGGCTGCACG AAAGCTTTCC CGAGAAGAGC CAGACCTCGG TCGTCATGCT CGATGGCGAA
GCCGACGTGC TTTCGAAAGG GCTCTTCTCG GTCTGGAGCC AGCAGTACGA GCTACCGCTT

       1330       1340       1350       1360       1370       1380
CAGGCGTTTC AGCGGGTCGA GGACCCGGAG GCGGAGATCT ATTGGGGCGC CTATCTCGGC
GTCCGCAAAG TCGCCCAGCT CCTGGGCCTC CGCCTCTAGA TAACCCCGCG GATAGAGCCG

       1390       1400       1410       1420       1430       1440
ACGCGGGATG AGATCGTCAT TTCCGGCCGC GTGGCTGAGG TGAAGGACCG GATCCTTGAA
TGCGCCCTAC TCTAGCAGTA AAGGCCGGCG CACCGACTCC ACTTCCTGGC CTAGGAACTT

       1450       1460       1470       1480       1490       1500
ACGCGGGCGG CGGCGCGCGC GAAGATGGGA TGGATCATGG ACATCTATCT CCTGCGCAAG
TGCGCCCGCC GCCGCGCGCG CTTCTACCCT ACCTAGTACC TGTAGATAGA GGACGCGTTC

       1510       1520       1530       1540       1550       1560
GGCGCCGACT TCGACGAGTG ACGGGGAGGG CCGATCTGCG TCGTGTTTGA TCTCACTCAA
CCGCGGCTGA AGCTGCTCAC TGCCCCTCCC GGCTAGACGC AGCACAAACT AGAGTGAGTT

       1570       1580       1590       1600       1610       1620
GGTTTGCGGC TGTGTTATAG CGTCTTAAGA GGCTTCTTCA GGGAGGAGAA CCTCAAGTGA
CCAAACGCCG ACACAATATC GCAGAATTCT CCGAAGAAGT CCCTCCTCTT GGAGTTCACT

       1630       1640       1650       1660       1670       1680
TGACGGATTT GATGACCAGC TGCGCCCTTC CATTGACCGG AGATGCCGGC ACCGTCGCTT
ACTGCCTAAA CTACTGGTCG ACGCGGGAAG GTAACTGGCC TCTACGGCCG TGGCAGCGAA

       1690       1700       1710       1720       1730       1740
CGATGCGCCG CGGCGCCTGC CCGTCCTTGG CAGAGCCGAT GCAGACCGGC GACGGCCTGC
GCTACGCGGC GCCGCGGACG GGCAGGAACC GTCTCGGCTA CGTCTGGCCG CTGCCGGACG

       1750       1760       1770       1780       1790       1800
TCGTGAGGGT GAGGCCAACG GATGACAGCC TGACGCTGCC GAAGGTCATT GCCCTTGCCA
AGCACTCCCA CTCCGGTTGC CTACTGTCGG ACTGCGACGG CTTCCAGTAA CGGGAACGGT
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FIG. 8C

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      1810       1820       1830       1840       1850       1860
CGGCTGCCGA GCGCTTCGGC AATGGCATCA TCGAGATTAC CGCGCGCGGA AACCTGCAGC
GCCGACGGCT CGCGAAGCCG TTACCGTAGT AGCTCTAATG GCGCGCGCCT TTGGACGTCG

      1870       1880       1890       1900       1910       1920
TTCGCGGCCT GAGCGCGGCT TCGGTGCCAA GGCTGGCGCA GGCGATCGGC GATGCGGAGA
AAGCGCCGGA CTCGCGCCGA AGCCACGGTT CCGACCGCGT CCGCTAGCCG CTACGCCTCT

      1930       1940       1950       1960       1970       1980
TCGCCATTGC CGAGGGGCTC GCGATCGAGG TGCCGCCCCT GGCCGGCATC GACCCGGACG
AGCGGTAACG GCTCCCCGAG CGCTAGCTCC ACGGCGGGGA CCGGCCGTAG CTGGGCCTGC

      1990       2000       2010       2020       2030       2040
AGATCGCCGA TCCGCGGCCG ATTGCCACTG AGCTTCGTGA AGCGTTGGAT GTGCGCCAGG
TCTAGCGGCT AGGCGCCGGC TAACGGTGAC TCGAAGCACT TCGCAACCTA CACGCGGTCC

      2050       2060       2070       2080       2090       2100
TGCCGTTGAA GCTTGCACCC AAATTATCCG TCGTCATCGA TAGCGGTGGC CGGTTTGGTC
ACGGCAACTT CGAACGTGGG TTTAATAGGC AGCAGTAGCT ATCGCCACCG GCCAAACCAG

      2110       2120       2130       2140       2150       2160
TCGGCGCTGT CGTCGCCGAC ATTCGCCTTC AGGCGGTTTC GACTGTCGCG GGGGTGGCCT
AGCCGCGACA GCAGCGGCTG TAAGCGGAAG TCCGCCAAAG CTGACAGCGC CCCCACCGGA

      2170       2180       2190       2200       2210       2220
GGGTGCTGTC GCTTGGCGGC ACGTCAACGA AGGCATCGAG CGTCGGGACG TTGGCCGGCA
CCCACGACAG CGAACCGCCG TGCAGTTGCT TCCGTAGCTC GCAGCCCTGC AACCGGCCGT

      2230       2240       2250       2260       2270       2280
ACGCGGTCGT GCCGGCCCTG ATCACCATTC TCGAGAAACT GGCGAGCCTG GGCACGACGA
TGCGCCAGCA CGGCCGGGAC TAGTGGTAAG AGCTCTTTGA CCGCTCGGAC CCGTGCTGCT

      2290       2300       2310       2320       2330       2340
TGCGCGGGCG CGATCTGGAC CCGTCGGAAA TCCGCGCGCT CTGTCGCTGT GAGACATCGT
ACGCGCCCGC GCTAGACCTG GGCAGCCTTT AGGCGCGCGA GACAGCGACA CTCTGTAGCA

      2350       2360       2370       2380       2390       2400
CCGAACGCCC GGCCGCTCCG CGTTCGGCCG CAATACCCGG CATTCATGCG CTGGGTAACG
GGCTTGCGGG CCGGCGAGGC GCAAGCCGGC GTTATGGGCC GTAAGTACGC GACCCATTGC
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FIG. 8D

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      2410       2420       2430       2440       2450       2460
CCGACACCGT TCTCGGCCTC GGTCTGGCCT TTGCTCAGGT GGAGGCCGCC GCGCTGGCAT
GGCTGTGGCA AGAGCCGGAG CCAGACCGGA AACGAGTCCA CCTCCGGCGG CGCGACCGTA

      2470       2480       2490       2500       2510       2520
CCTACCTGCA TCAGGTCCAG GCGCTTGGCG CCAATGCGAT CCGGCTTGCG CCCGGGCACG
GGATGGACGT AGTCCAGGTC CGCGAACCGC GGTTACGCTA GGCCGAACGC GGGCCCGTGC

      2530       2540       2550       2560       2570       2580
CCTTCTTCGT CCTCGGCCTT TGCCCCGAGA CCGCGGCTGT GGCGCAGAGC CTGGCAGCGT
GGAAGAAGCA GGAGCCGGAA ACGGGGCTCT GGCGCCGACA CCGCGTCTCG GACCGTCGCA

      2590       2600       2610       2620       2630       2640
CACACGGTTT TCGCATTGCC GAGCAGGATC CGCGCAATGC GATCGCCACC TGCGCCGGCA
GTGTGCCAAA AGCGTAACGG CTCGTCCTAG GCGCGTTACG CTAGCGGTGG ACGCGGCCGT

      2650       2660       2670       2680       2690       2700
GCAAGGGTTG CGCCTCGGCG TGGATGGAAA CCAAGGGCAT GGCCGAGCGC CTCGTCGAGA
CGTTCCCAAC GCGGAGCCGC ACCTACCTTT GGTTCCCGTA CCGGCTCGCG GAGCAGCTCT

      2710       2720       2730       2740       2750       2760
CGGCGCCGGA ATTGCTCGAC GGGTCGCTCA CCGTGCATCT CTCCGGCTGC GCCAAGGGCT
GCCGCGGCCT TAACGAGCTG CCCAGCGAGT GGCACGTAGA GAGGCCGACG CGGTTCCCGA

      2770       2780       2790       2800       2810       2820
GCGCCCGGCC GAAGCCGTCC GAACTGACGC TTGTCGGTGC GCCATCAGGA TACGGGCTTG
CGCGGGCCGG CTTCGGCAGG CTTGACTGCG AACAGCCACG CGGTAGTCCT ATGCCCGAAC

      2830       2840       2850       2860       2870       2880
TCGTAAATGG GGCTGCCAAT GGCTTGCCAA GCGCCTACAC CGATGAGAAT GGAATGGGAT
AGCATTTACC CCGACGGTTA CCGAACGGTT CGCGGATGTG GCTACTCTTA CCTTACCCTA

      2890       2900       2910       2920       2930       2940
CCGCCCTTGC CCGGCTCGGC CGGCTGGTGC GGCAAAACAA AGACGCTGGC GAATCGGCGC
GGCGGGAACG GGCCGAGCCG GCCGACCACG CCGTTTTGTT TCTGCGACCG CTTAGCCGCG

      2950       2960       2970       2980       2990       3000
AGTCCTGTCT TACACGGCTC GGAGCTGCGC GCGTCTCGGC AGCGTTCGAA CAGGGATAGA
TCAGGACAGA ATGTGCCGAG CCTCGACGCG CGCAGAGCCG TCGCAAGCTT GTCCCTATCT
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FIG. 8E

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      3010       3020       3030       3040       3050       3060
CATGCCTGAG TATGATTACA TTCGCGATGG CAACGCCATC TACGAGCGTT CCTTCGCCAT
GTACGGACTC ATACTAATGT AAGCGCTACC GTTGCGGTAG ATGCTCGCAA GGAAGCGGTA

      3070       3080       3090       3100       3110       3120
CATCCGCGCC GAGGCCGATC TGTCGCGCTT CTCCGAAGAG GAAGCGGATC TGGCTGTGCG
GTAGGCGCGG CTCCGGCTAG ACAGCGCGAA GAGGCTTCTC CTTCGCCTAG ACCGACACGC

      3130       3140       3150       3160       3170       3180
CATGGTGCAC GCCTGCGGTT CCGTCGAGGC GACCAGGCAG TTCGTGTTTT CTCCCGATTT
GTACCACGTG CGGACGCCAA GGCAGCTCCG CTGGTCCGTC AAGCACAAAA GAGGGCTAAA

      3190       3200       3210       3220       3230       3240
CGTAAGCTCG GCCCGTGCGG CGCTGAAAGC CGGTGCGCCG ATCCTCTGCG ATGCCGAGAT
GCATTCGAGC CGGGCACGCC GCGACTTTCG GCCACGCGGC TAGGAGACGC TACGGCTCTA

      3250       3260       3270       3280       3290       3300
GGTTGCGCAC GGTGTCACCC GCGCCCGTCT GCCGGCCGGC AACGAGGTGA TCTGCACGCT
CCAACGCGTG CCACAGTGGG CGCGGGCAGA CGGCCGGCCG TTGCTCCACT AGACGTGCGA

      3310       3320       3330       3340       3350       3360
GCGCGATCCT CGCACGCCCG CACTTGCGGC CGAGATCGGC AACACCCGCT CCGCCGCAGC
CGCGCTAGGA GCGTGCGGGC GTGAACGCCG GCTCTAGCCG TTGTGGGCGA GGCGGCGTCG

      3370       3380       3390       3400       3410       3420
CCTGAAGCTC TGGAGCGAGC GGCTGGCCGG TTCGGTGGTC GCGATCGGCA ACGCGCCGAC
GGACTTCGAG ACCTCGCTCG CCGACCGGCC AAGCCACCAG CGCTAGCCGT TGCGCGGCTG

      3430       3440       3450       3460       3470       3480
GGCGTTGTTC TTCCTCTTGG AAATGCTGCG CGACGGCGCG CCGAAGCCGG CGGCAATCCT
CCGCAACAAG AAGGAGAACC TTTACGACGC GCTGCCGCGC GGCTTCGGCC GCCGTTAGGA

      3490       3500       3510       3520       3530       3540
CGGCATGCCC GTCGGTTTCG TCGGTGCGGC GGAATCGAAG GATGCGCTGG CCGAGAACTC
GCCGTACGGG CAGCCAAAGC AGCCACGCCG CCTTAGCTTC CTACGCGACC GGCTCTTGAG

      3550       3560       3570       3580       3590       3600
CTATGGCGTT CCCTTCGCCA TCGTGCGCGG CCGCCTCGGC GGGAGTGCCA TGACGGCGGC
GATACCGCAA GGGAAGCGGT AGCACGCGCC GGCGGAGCCG CCCTCACGGT ACTGCCGCCG
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FIG. 8F

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      3610       3620       3630       3640       3650       3660
AGCGCTTAAC TCGCTCGCGA GGCCGGGCCT GTGAGCGGCG TCGGCGTGGG GCGCCTGATC
TCGCGAATTG AGCGAGCGCT CCGGCCCGGA CACTCGCCGC AGCCGCACCC CGCGGACTAG

      3670       3680       3690       3700       3710       3720
GGTGTTGGGA CCGGCCCCGG TGATCCGGAA CTTTTGACGG TCAAGGCGGT GAAGGCGCTC
CCACAACCCT GGCCGGGGCC ACTAGGCCTT GAAAACTGCC AGTTCCGCCA CTTCCGCGAG

      3730       3740       3750       3760       3770       3780
GGGCAAGCCG ATGTGCTTGC CTATTTCGCC AAGGCCGGGC GAAGCGGTAA CGGCCGCGCG
CCCGTTCGGC TACACGAACG GATAAAGCGG TTCCGGCCCG CTTCGCCATT GCCGGCGCGC

      3790       3800       3810       3820       3830       3840
GTGGTCGAGG GTCTGCTGAA GCCCGATCTT GTCGAGCTGC CGCTATACTA TCCGGTGACG
CACCAGCTCC CAGACGACTT CGGGCTAGAA CAGCTCGACG GCGATATGAT AGGCCACTGC

      3850       3860       3870       3880       3890       3900
ACCGAAATCG ACAAGGACGA TGGCGCCTAC AAGACCCAGA TCACCGACTT CTACAATGCG
TGGCTTTAGC TGTTCCTGCT ACCGCGGATG TTCTGGGTCT AGTGGCTGAA GATGTTACGC

      3910       3920       3930       3940       3950       3960
TCGGCCGAAG CGGTAGCGGC GCATCTTGCC GCCGGGCGCA CGGTCGCCGT GCTCAGTGAA
AGCCGGCTTC GCCATCGCCG CGTAGAACGG CGGCCCGCGT GCCAGCGGCA CGAGTCACTT

      3970       3980       3990       4000       4010       4020
GGCGACCCGC TGTTCTATGG TTCCTACATG CATCTGCATG TGCGGCTCGC CAATCGTTTC
CCGCTGGGCG ACAAGATACC AAGGATGTAC GTAGACGTAC ACGCCGAGCG GTTAGCAAAG

      4030       4040       4050       4060       4070       4080
CCGGTCGAGG TGATCCCCGG CATTACCGCC ATGTCCGGCT GTTGGTCGCT TGCCGGCCTG
GGCCAGCTCC ACTAGGGGCC GTAATGGCGG TACAGGCCGA CAACCAGCGA ACGGCCGGAC

      4090       4100       4110       4120       4130       4140
CCGCTGGTGC AGGGCGACGA CGTGCTCTCG GTGCTTCCGG GCACCATGGC CGAGGCCGAG
GGCGACCACG TCCCGCTGCT GCACGAGAGC CACGAAGGCC CGTGGTACCG GCTCCGGCTC

      4150       4160       4170       4180       4190       4200
CTCGGCCGCA GGCTTGCGGA TACCGAAGCC GCCGTGATCA TGAAGGTCGG GCGCAATTTG
GAGCCGGCGT CCGAACGCCT ATGGCTTCGG CGGCACTAGT ACTTCCAGCC CGCGTTAAAC
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FIG. 8G

4210 4220 4230 4240 4250 4260
CCGAAGATCC GTCGGGCGCT CGCTGCCTCC GGCCGTCTCG ACCAGGCCGT CTATGTCGAA
GGCTTCTAGG CAGCCCGCGA GCGACGGAGG CCGGCAGAGC TGGTCCGGCA GATACAGCTT

4270 4280 4290 4300 4310 4320
CGCGGCACGA TGAAGAACGC GGCGATGACG GCTCTTGCGG AAAAGGCCGA CGACGAGGCG
GCGCCGTGCT ACTTCTTGCG CCGCTACTGC CGAGAACGCC TTTTCCGGCT GCTGCTCCGC

4330 4340 4350 4360 4370 4380
CCCTATTTCT CGCTGGTGCT CGTTCCCGGC TGGAAGGACC GACCATGACC GGTACGCTCT
GGGATAAAGA GCGACCACGA GCAAGGGCCG ACCTTCCTGG CTGGTACTGG CCATGCGAGA

4390 4400 4410 4420 4430 4440
ATGTCGTCGG TACCGGACCG GGCAGCGCCA AGCAGATGAC GCCGGAAACG GCGGAAGCCG
TACAGCAGCC ATGGCCTGGC CCGTCGCGGT TCGTCTACTG CGGCCTTTGC CGCCTTCGGC

4450 4460 4470 4480 4490 4500
TTGCGGCCGC TCAGGAGTTT TACGGCTACT TTCCCTATCT CGACCGGCTG AACCTCAGAC
AACGCCGGCG AGTCCTCAAA ATGCCGATGA AAGGGATAGA GCTGGCCGAC TTGGAGTCTG

4510 4520 4530 4540 4550 4560
CGGATCAGAT CCGTGTCGCC TCGGACAACC GCGAGGAGCT CGATCGGGCA CAGGTCGCGC
GCCTAGTCTA GGCACAGCGG AGCCTGTTGG CGCTCCTCGA GCTAGCCCGT GTCCAGCGCG

4570 4580 4590 4600 4610 4620
TGACGCGGGC TGCGGCAGGC GTGAAGGTCT GCATGGTCTC CGGTGGCGAT CCCGGTGTCT
ACTGCGCCCG ACGCCGTCCG CACTTCCAGA CGTACCAGAG GCCACCGCTA GGGCCACAGA

4630 4640 4650 4660 4670 4680
TTGCCATGGC GGCCGCCGTC TGCGAGGCGA TCGACAAGGG ACCGGCGGAA TGGAAGTCGG
AACGGTACCG CCGGCGGCAG ACGCTCCGCT AGCTGTTCCC TGGCCGCCTT ACCTTCAGCC

4690 4700 4710 4720 4730 4740
TTGAACTGGT GATCACGCCC GGCGTGACCG CGATGCTCGC CGTTGCCGCC CGCATCGGCG
AACTTGACCA CTAGTGCGGG CCGCACTGGC GCTACGAGCG GCAACGGCGG GCGTAGCCGC

4750 4760 4770 4780 4790 4800
CGCCGCTCGG TCATGATTTC TGTGCGATCT CGCTTTCCGA CAATCTGAAG CCCTGGGAAG
GCGGCGAGCC AGTACTAAAG ACACGCTAGA GCGAAAGGCT GTTAGACTTC GGGACCCTTC

FIG. 8H

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      4810       4820       4830       4840       4850       4860
TCATCACCCG GCGTCTCAGG CTGGCGGCGG AAGCGGGCTT CGTCATTGCC CTCTACAATC
AGTAGTGGGC CGCAGAGTCC GACCGCCGCC TTCGCCCGAA GCAGTAACGG GAGATGTTAG

      4870       4880       4890       4900       4910       4920
CGATCAGCAA GGCGCGGCCC TGGCAGCTCG GTGAGGCCTT CGAGCTTCTG CGCAGCGTTC
GCTAGTCGTT CCGCGCCGGG ACCGTCGAGC CACTCCGGAA GCTCGAAGAC GCGTCGCAAG

      4930       4940       4950       4960       4970       4980
TGCCGGCAAG CGTTCCGGTC ATCTTCGGCC GTGCGGCCGG GCGGCCGGAC GAACGGATCG
ACGGCCGTTC GCAAGGCCAG TAGAAGCCGG CACGCCGGCC CGCCGGCCTG CTTGCCTAGC

      4990       5000       5010       5020       5030       5040
CGGTGATGCC GCTCGGCGAG GCCGATGCCA ACCGCGCCGA CATGGCGACC TGCGTCATCA
GCCACTACGG CGAGCCGCTC CGGCTACGGT TGGCGCGGCT GTACCGCTGG ACGCAGTAGT

      5050       5060       5070       5080       5090       5100
TCGGCTCGCC GGAGACGCGC ATCGTCGAGC GCGACGGCCA ACCCGATCTC GTCTACACAC
AGCCGAGCGG CCTCTGCGCG TAGCAGCTCG CGCTGCCGGT TGGGCTAGAG CAGATGTGTG

      5110       5120       5130       5140       5150       5160
CGCGCTTCTA TGCAGGGGCG AGCCAGTGAG CGATGCGGTT GAGTGCCTCG TCGCAACTGC
GCGCGAAGAT ACGTCCCCGC TCGGTCACTC GCTACGCCAA CTCACGGAGC AGCGTTGACG

      5170       5180       5190       5200       5210       5220
CGACCGTCGG CACGTCCGCG GGCTTGCGCC GCTCGACCAT GATCACCTCG ATGCCGAGCC
GCTGGCAGCC GTGCAGGCGC CCGAACGCGG CGAGCTGGTA CTAGTGGAGC TACGGCTCGG

      5230       5240       5250       5260       5270       5280
GGCGCGCTGC GGCAATCTTG CCGTAGGTGG CGCTGCCACC GCTGTTCTTG GCGACGATCA
CCGCGCGACG CCGTTAGAAC GGCATCCACC GCGACGGTGG CGACAAGAAC CGCTGCTAGT

      5290       5300       5310       5320       5330       5340
CATCGATCTG CCGACTCCTG AGCAACGCGG CTTCGTCGGC TTCCGCAAAG GGACCGGTCG
GTAGCTAGAC GGCTGAGGAC TCGTTGCGCC GAAGCAGCCG AAGGCGTTTC CCTGGCCAGC

      5350       5360       5370       5380       5390       5400
CCAGGATCGC CTCCTGGTCG GGCAGATTAA GCGGCGGCGT CACCGGATCG ACGCTGCGGA
GGTCCTAGCG GAGGACCAGC CCGTCTAATT CGCCGCCGCA GTGGCCTAGC TGCGACGCCT
```

FIG. 8I

```
      5410       5420       5430       5440       5450       5460
TGACGTAGCT GTGCTGCGGC GCGACCTCGA AGTGGAAAGC TTCCTGTCGA CCTATCGCCA
ACTGCATCGA CACGACGCCG CGCTGGAGCT TCACCTTTCG AAGGACAGCT GGATAGCGGT

      5470       5480       5490       5500       5510       5520
GGAAGACGCG GCGTCGCCGA TCACCGAGCG CGCTGACGGC CTCGACAACG CTATCGACAG
CCTTCTGCGC CGCAGCGGCT AGTGGCTCGC GCGACTGCCG GAGCTGTTGC GATAGCTGTC

      5530       5540       5550       5560       5570       5580
CAGTCCAGCG GTCGCCAGGC AGGGGCACCC ATTCCGGTCG GCGGAGGGCG ATAAGCGCAA
GTCAGGTCGC CAGCGGTCCG TCCCCGTGGG TAAGGCCAGC CGCCTCCCGC TATTCGCGTT

      5590       5600       5610       5620       5630       5640
CGCCGGTTCT TTGCGCTGCG TCCGCGGCGT TGTGCGAAAT GCGTGCGGCA AAGGGGTGCG
GCGGCCAAGA AACGCGACGC AGGCGCCGCA ACACGCTTTA CGCACGCCGT TTCCCCACGC

      5650       5660       5670       5680       5690       5700
TCGCATCGAC CAGCAGCGCG ATGTTTTCGT CATGCACGAA ATGCGCCAGC CCATCGGCGC
AGCGTAGCTG GTCGTCGCGC TACAAAAGCA GTACGTGCTT TACGCGGTCG GGTAGCCGCG

      5710       5720       5730       5740       5750       5760
CGCCAAAGCC GCCGATGCGC GTCTTGACCG GCTGCGGCCG CGGGTCCGCG GTGCGGCCGG
GCGGTTTCGG CGGCTACGCG CAGAACTGGC CGACGCCGGC GCCCAGGCGC CACGCCGGCC

      5770       5780       5790       5800       5810       5820
CCAGCGAGAT GGCGGTGTCG TAGCGGACAT CTTCGGCCAA GCGGCGCGCG AGTTCGCGTG
GGTCGCTCTA CCGCCACAGC ATCGCCTGTA GAAGCCGGTT CGCCGCGCGC TCAAGCGCAC

      5830       5840       5850       5860       5870       5880
CCTCGGTGGT GCCACCCAGA ATCAGAATAC GAGGTTTTTC CATGGCTGAC GTGTCGAACA
GGAGCCACCA CGGTGGGTCT TAGTCTTATG CTCCAAAAAG GTACCGACTG CACAGCTTGT

      5890       5900       5910       5920       5930       5940
GCGAACCCGC CATAGTCTCC CCCTGGCTGA CCGTCATCGG TATCGGTGAG GATGGTGTAG
CGCTTGGGCG GTATCAGAGG GGGACCGACT GGCAGTAGCC ATAGCCACTC CTACCACATC

      5950       5960       5970       5980       5990       6000
CGGGTCTCGG CGACGAGGCC AAGCGGCTGA TCGCCGAAGC GCCGGTCGTC TACGGCGGCC
GCCCAGAGCC GCTGCTCCGG TTCGCCGACT AGCGGCTTCG CGGCCAGCAG ATGCCGCCGG
```

FIG. 8J

```
      6010       6020       6030       6040       6050       6060
ATCGTCATCT GGAGCTCGCC GCCTCCCTCA TCACCGGCGA AGCGCACAAT TGGCTAAGCC
TAGCAGTAGA CCTCGAGCGG CGGAGGGAGT AGTGGCCGCT TCGCGTGTTA ACCGATTCGG

      6070       6080       6090       6100       6110       6120
CCCTCGAACG CTCGGTCGTC GAGATCGTCG CGCGTCGCGG CAGCCCGGTG GTGGTGCTTG
GGGAGCTTGC GAGCCAGCAG CTCTAGCAGC GCGCAGCGCC GTCGGGCCAC CACCACGAAC

      6130       6140       6150       6160       6170       6180
CCTCGGGCGA CCCGTTCTTC TTCGGCGTCG GCGTGACGCT GGCGCGCCGC ATCGCCTCGG
GGAGCCCGCT GGGCAAGAAG AAGCCGCAGC CGCACTGCGA CCGCGCGGCG TAGCGGAGCC

      6190       6200       6210       6220       6230       6240
CCGAAATACG CACGCTTCCG GCGCCGTCGT CGATCAGTCT TGCCGCCTCG CGCCTCGGCT
GGCTTTATGC GTGCGAAGGC CGCGGCAGCA GCTAGTCAGA ACGGCGGAGC GCGGAGCCGA

      6250       6260       6270       6280       6290       6300
GGGCGCTGCA GGATGCGACG CTCGTCTCCG TACATGGGCG GCCGCTGGAT CTGGTGCGAC
CCCGCGACGT CCTACGCTGC GAGCAGAGGC ATGTACCCGC CGGCGACCTA GACCACGCTG

      6310       6320       6330       6340       6350       6360
CGCATTTGCA TCCGGGGGCG CGTGTGCTTA CGCTCACGTC GGACGGTGCG GGTCCGCGAG
GCGTAAACGT AGGCCCCCGC GCACACGAAT GCGAGTGCAG CCTGCCACGC CCAGGCGCTC

      6370       6380       6390       6400       6410       6420
ACCTTGCCGA GCTTCTGGTT TCAAGCGGCT TCGGTCAGTC GCGACTGACC GTGCTCGAAG
TGGAACGGCT CGAAGACCAA AGTTCGCCGA AGCCAGTCAG CGCTGACTGG CACGAGCTTC

      6430       6440       6450       6460       6470       6480
CGCTGGGCGG CGCCGGCGAA CGGGTGACGA CGCAGATCGC CGCGCGCTTC ATGCTCGGCC
GCGACCCGCC GCGGCCGCTT GCCCACTGCT GCGTCTAGCG GCGCGCGAAG TACGAGCCGG

      6490       6500       6510       6520       6530       6540
TCGTGCATCC TTTGAACGTC TGCGCCATTG AGGTGGCGGC CGACGAGGGC GCGCGCATCC
AGCACGTAGG AAACTTGCAG ACGCGGTAAC TCCACCGCCG GCTGCTCCCG CGCGCGTAGG

      6550       6560       6570       6580       6590       6600
TGCCGCTTGC CGCCGGCCGC GACGATGCGC TGTTCGAACA TGACGGGCAG ATCACCAAGC
ACGGCGAACG GCGGCCGGCG CTGCTACGCG ACAAGCTTGT ACTGCCCGTC TAGTGGTTCG
```

FIG. 8K

```
      6610       6620       6630       6640       6650       6660
GCGAGGTGCG GGCGCTGACG CTGTCGGCAC TCGCACCGCG CAAGGGCGAA CTGCTATGGG
CGCTCCACGC CCGCGACTGC GACAGCCGTG AGCGTGGCGC GTTCCCGCTT GACGATACCC

      6670       6680       6690       6700       6710       6720
ACATCGGCGG CGGCTCCGGC TCGATCGGCA TCGAATGGAT GCTCGCCGAT CCGACCATGC
TGTAGCCGCC GCCGAGGCCG AGCTAGCCGT AGCTTACCTA CGAGCGGCTA GGCTGGTACG

      6730       6740       6750       6760       6770       6780
AGGCGATCAC CATCGAGGTT GAGCCGGAGC GGGCAGCGCG CATCGGCCGC AACGCGACGA
TCCGCTAGTG GTAGCTCCAA CTCGGCCTCG CCCGTCGCGC GTAGCCGGCG TTGCGCTGCT

      6790       6800       6810       6820       6830       6840
TGTTCGGCGT GCCCGGGCTG ACGGTTGTCG AAGGCGAGGC GCCGGCGGCG CTTGCCGGCC
ACAAGCCGCA CGGGCCCGAC TGCCAACAGC TTCCGCTCCG CGGCCGCCGC GAACGGCCGG

      6850       6860       6870       6880       6890       6900
TGCCACAACC GGACGCGATC TTCATCGGCG GCGGCGGCAG CGAAGACGGC GTCATGGAAG
ACGGTGTTGG CCTGCGCTAG AAGTAGCCGC CGCCGCCGTC GCTTCTGCCG CAGTACCTTC

      6910       6920       6930       6940       6950       6960
CAGCGATCGA GGCGCTCAAG TCAGGCGGAC GGCTGGTTGC CAACGCGGTG ACGACGGACA
GTCGCTAGCT CCGCGAGTTC AGTCCGCCTG CCGACCAACG GTTGCGCCAC TGCTGCCTGT

      6970       6980       6990       7000       7010       7020
TGGAAGCGGT GCTGCTCGAT CATCACGCGC GGCTCGGCGG TTCGCTGATC CGCATCGATA
ACCTTCGCCA CGACGAGCTA GTAGTGCGCG CCGAGCCGCC AAGCGACTAG GCGTAGCTAT

      7030       7040       7050       7060       7070       7080
TCGCGCGTGC AGGACCCATC GGCGGCATGA CCGGCTGGAA GCCGGCCATG CCGGTCACCC
AGCGCGCACG TCCTGGGTAG CCGCCGTACT GGCCGACCTT CGGCCGGTAC GGCCAGTGGG

      7090       7100       7110       7120       7130       7140
AATGGTCGTG GACGAAGGGC TAAAGCAGTT CCAGCGAAAG TGTGACGCGG TTTTGCGTCC
TTACCAGCAC CTGCTTCCCG ATTTCGTCAA GGTCGCTTTC ACACTGCGCC AAAACGCAGG

      7150       7160       7170       7180       7190       7200
GGAACTGCGC AAGAAAAAGA AAGAGTAACC TATGACGGTA CATTTCATCG GCGCCGGCCC
CCTTGACGCG TTCTTTTTCT TTCTCATTGG ATACTGCCAT GTAAAGTAGC CGCGGCCGGG
```

FIG. 8L

```
      7210       7220       7230       7240       7250       7260
GGGAGCCGCA GACCTGATCA CGGTGCGTGG TCGCGACCTG ATCGGGCGCT GCCCGGTCTG
CCCTCGGCGT CTGGACTAGT GCCACGCACC AGCGCTGGAC TAGCCCGCGA CGGGCCAGAC

      7270       7280       7290       7300       7310       7320
CCTTTACGCC GGCTCGATCG TCTCGCCGGA GCTGCTGCGA TATTGCCCGC CGGGCGCCCG
GGAAATGCGG CCGAGCTAGC AGAGCGGCCT CGACGACGCT ATAACGGGCG GCCCGCGGGC

      7330       7340       7350       7360       7370       7380
CATTGTCGAT ACGGCGCCGA TGTCCCTCGA CGAGATCGAG GCGGAGTATG TGAAGGCCGA
GTAACAGCTA TGCCGCGGCT ACAGGGAGCT GCTCTAGCTC CGCCTCATAC ACTTCCGGCT

      7390       7400       7410       7420       7430       7440
AGCCGAAGGG CTCGACGTGG CGCGGCTTCA TTCGGGCGAC CTTTCGGTCT GGAGTGCTGT
TCGGCTTCCC GAGCTGCACC GCGCCGAAGT AAGCCCGCTG GAAAGCCAGA CCTCACGACA

      7450       7460       7470       7480       7490       7500
GGCCGAACAG ATCCGCCGGC TCGAGAAGCA TGGCATCGCC TATACGATGA CGCCGGGCGT
CCGGCTTGTC TAGGCGGCCG AGCTCTTCGT ACCGTAGCGG ATATGCTACT GCGGCCCGCA

      7510       7520       7530       7540       7550       7560
TCCTTCCTTT GCGGCGGCGG CTTCAGCGCT CGGTCGCGAA TTGACCATTC CGGCCGTGGC
AGGAAGGAAA CGCCGCCGCC GAAGTCGCGA GCCAGCGCTT AACTGGTAAG GCCGGCACCG

      7570       7580       7590       7600       7610       7620
CCAGAGCCTG GTGCTGACCC GCGTTTCGGG CCGCGCCTCG CCGATGCCGA ACTCAGAAAC
GGTCTCGGAC CACGACTGGG CGCAAAGCCC GGCGCGGAGC GGCTACGGCT TGAGTCTTTG

      7630       7640       7650       7660       7670       7680
GCTTTCCGCT TTCGGCGCTA CGGGATCGAC GCTGGCAATC CACCTTGCGA TCCATGCGCT
CGAAAGGCGA AAGCCGCGAT GCCCTAGCTG CGACCGTTAG GTGGAACGCT AGGTACGCGA

      7690       7700       7710       7720       7730       7740
TCAGCAGGTG GTCGAGGAAC TGACGCCGCT CTACGGTGCC GACTGCCCGG TCGCCATCGT
AGTCGTCCAC CAGCTCCTTG ACTGCGGCGA GATGCCACGG CTGACGGGCC AGCGGTAGCA

      7750       7760       7770       7780       7790       7800
CGTCAAGGCC TCCTGGCCGG ACGAACGCGT GGTGCGCGGC ACGCTCGGTG ACATCGCCGC
GCAGTTCCGG AGGACCGGCC TGCTTGCGCA CCACGCGCCG TGCGAGCCAC TGTAGCGGCG
```

FIG. 8M

```
      7810       7820       7830       7840       7850       7860
CAAGGTGGCG GAAGAGCCGA TCGAGCGCAC GGCGCTGATC TTCGTCGGTC CGGGGCTCGA
GTTCCACCGC CTTCTCGGCT AGCTCGCGTG CCGCGACTAG AAGCAGCCAG GCCCCGAGCT

      7870       7880       7890       7900       7910       7920
AGCCTCCGAT TTCCGTGAAA GCTCGCTCTA CGATCCCGCC TATCAGCGGC GCTTCAGAGG
TCGGAGGCTA AAGGCACTTT CGAGCGAGAT GCTAGGGCGG ATAGTCGCCG CGAAGTCTCC

      7930       7940       7950       7960       7970       7980
GCGCGGCGAA TAGGCCGCAC TCCCTCGGGG GTCGGCCTAA GTTTCCCGCT GAGAGGGTTT
CGCGCCGCTT ATCCGGCGTG AGGGAGCCCC CAGCCGGATT CAAAGGGCGA CTCTCCCAAA

      7990       8000       8010       8020       8030       8040
TGAAACCTAT TCTGCCGGTT CTTCGCGCGG CGGCCGCTGC TTGAGCGGGA CGCCGCGCTT
ACTTTGGATA AGACGGCCAA GAAGCGCGCC GCCGGCGACG AACTCGCCCT GCGGCGCGAA

      8050       8060       8070       8080       8090       8100
TTCCTCGACG CGGTCGCGGT AGAGCGCTGC CTGTCCAAGC AGCATCAGCG TCACCGGCGT
AAGGAGCTGC GCCAGCGCCA TCTCGCGACG GACAGGTTCG TCGTAGTCGC AGTGGCCGCA

      8110       8120       8130       8140       8150       8160
GGTGGCGACG ACGAAGACGA TGATCAGGAT TTCGTGGAAT ACCCAGCGGC TCTGCAGCAC
CCACCGCTGC TGCTTCTGCT ACTAGTCCTA AAGCACCTTA TGGGTCGCCG AGACGTCGTG

      8170       8180       8190       8200       8210       8220
GGCAAAGCAG ATGATAGAGG CGGCGCAGAT CATCAGTACG CCGCCGCTGG TCGCCAGCGT
CCGTTTCGTC TACTATCTCC GCCGCGTCTA GTAGTCATGC GGCGGCGACC AGCGGTCGCA

      8230       8240       8250       8260       8270       8280
CGGTGCGTGC AGGCGCTCGT AGAAGCTGGT GAACCGGAGC AAGCCGACGG AGCCGATCAG
GCCACGCACG TCCGCGAGCA TCTTCGACCA CTTGGCCTCG TTCGGCTGCC TCGGCTAGTC

      8290       8300       8310       8320       8330       8340
CGCCACTGCG GCGCCGAGGA CGGTGAGCCC GCAGACGAGA ACGGCTGCCC AGACGGGAAG
GCGGTGACGC CGCGGCTCCT GCCACTCGGG CGTCTGCTCT TGCCGACGGG TCTGCCCTTC

      8350       8360       8370       8380       8390       8400
GTCGGTGAGG TGGCTCATTC GATGATCTCC CCGCGCATCA GGAACTTGCC GAAGGCGATC
CAGCCACTCC ACCGAGTAAG CTACTAGAGG GGCGCGTAGT CCTTGAACGG CTTCCGCTAG
```

FIG. 8N

```
      8410       8420       8430       8440       8450       8460
GACGAGACGA AGCCGATCAA AGCCACGATC AGGGCGGACT CGAAATAGAG CGAGTTGGCC
CTGCTCTGCT TCGGCTAGTT TCGGTGCTAG TCCCGCCTGA GCTTTATCTC GCTCAACCGG

      8470       8480       8490       8500       8510       8520
GTGCGGATGC CGAAGGTCAA GAGCATCAGC ATGGCGTTGA TATAGAGCGT GTCGAGGCCG
CACGCCTACG GCTTCCAGTT CTCGTAGTCG TACCGCAACT ATATCTCGCA CAGCTCCGGC

      8530       8540       8550       8560       8570       8580
AGGATACGGT CCTGGGCGCG CGGTCCCCTC ACCATGCGAT AGAAGGCAAA AGCCATCGCC
TCCTATGCCA GGACCCGCGC GCCAGGGGAG TGGTACGCTA TCTTCCGTTT TCGGTAGCGG

      8590       8600       8610       8620       8630       8640
AGGCCGAGCA TGATCTGGGC AATCAGGATC GACCAGATGA TTGAAAGTTC CATCATCCGA
TCCGGCTCGT ACTAGACCCG TTAGTCCTAG CTGGTCTACT AACTTTCAAG GTAGTAGGCT

      8650       8660       8670       8680       8690       8700
ATATCTCCTT CAGGGCGGTC TCATAGCGCT TGACCGTATC GAGCCAGATG TCCTCGTTCT
TATAGAGGAA GTCCCGCCAG AGTATCGCGA ACTGGCATAG CTCGGTCTAC AGGAGCAAGA

      8710       8720       8730       8740       8750       8760
CCATGTCGAG CACGTGGAAG AGCAGGGACT TGCGGCCGCG ATCCGGGGAA TTC
GGTACAGCTC GTGCACCTTC TCGTCCCTGA ACGCCGGCGC TAGGCCCCTT AAG
```

FIG. 8O

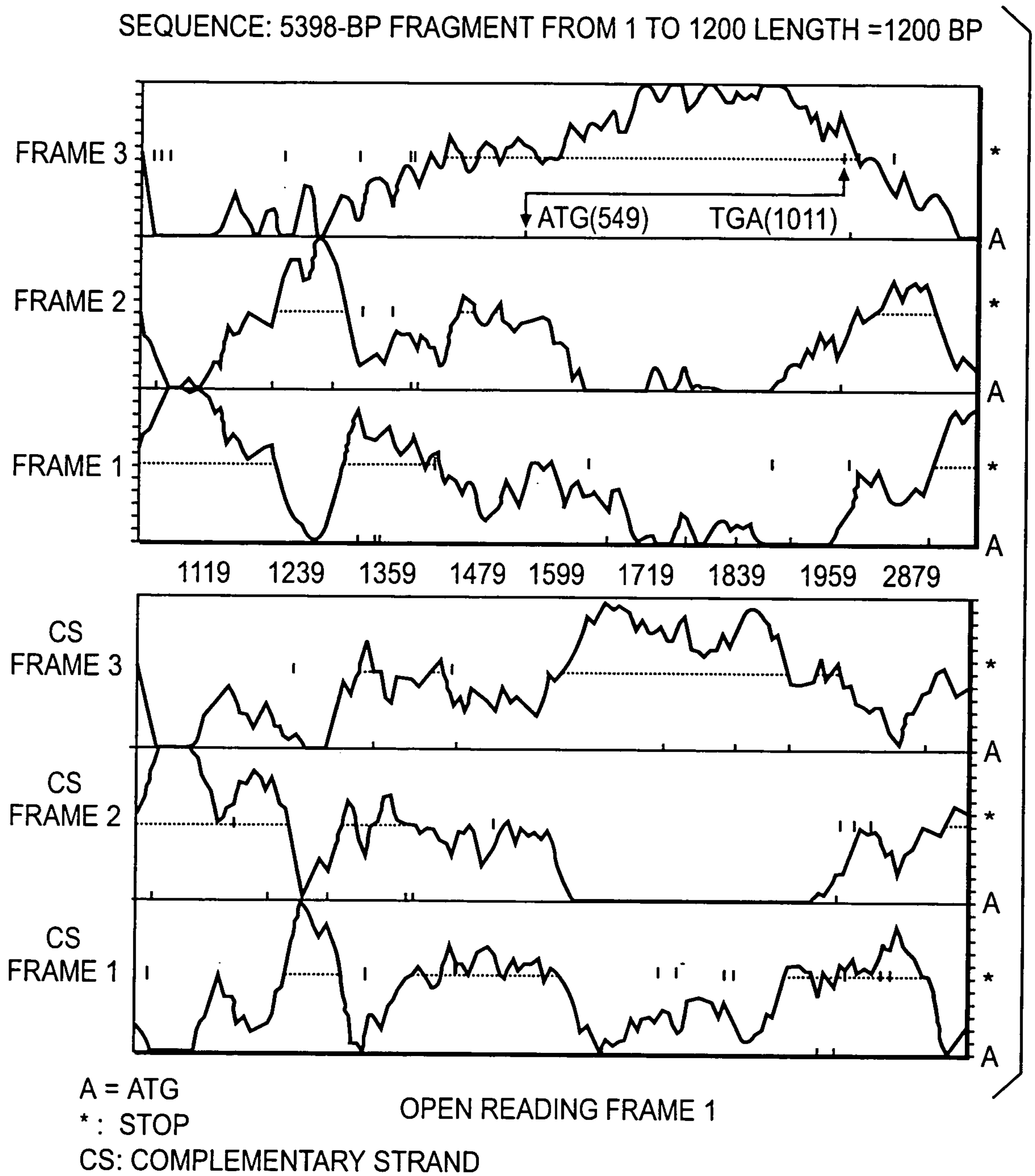

SEQUENCE: 5398-BP FRAGMENT FROM 1 TO 1200 LENGTH =1200 BP
FRAME 3
FRAME 2
FRAME 1
ATG(549)
TGA(1011)
A
*
1119
1239
1359
1479
1599
1719
1839
1959
2879
CS FRAME 3
CS FRAME 2
CS FRAME 1
A = ATG
*: STOP
CS: COMPLEMENTARY STRAND
OPEN READING FRAME 1

FIG. 9A

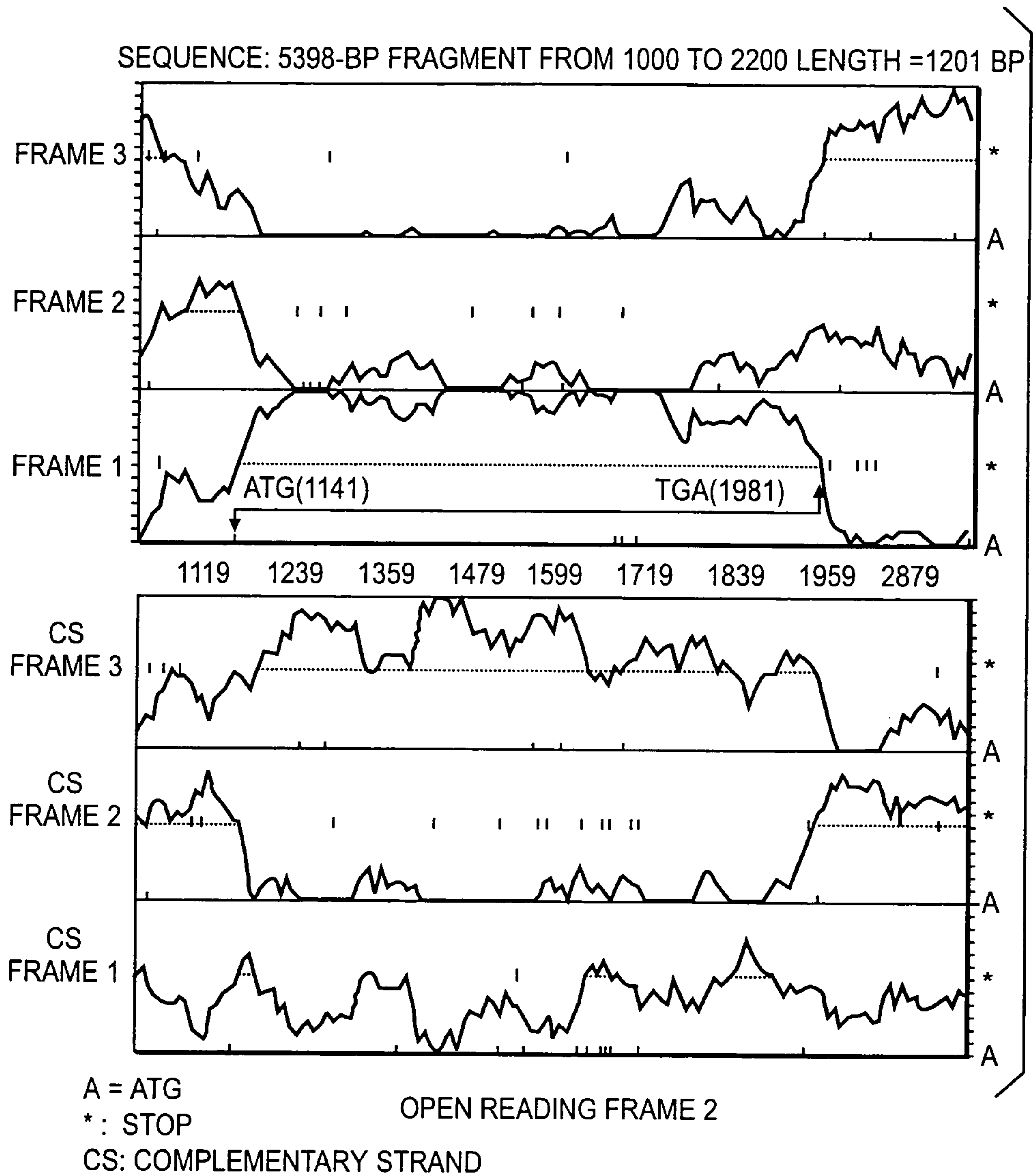
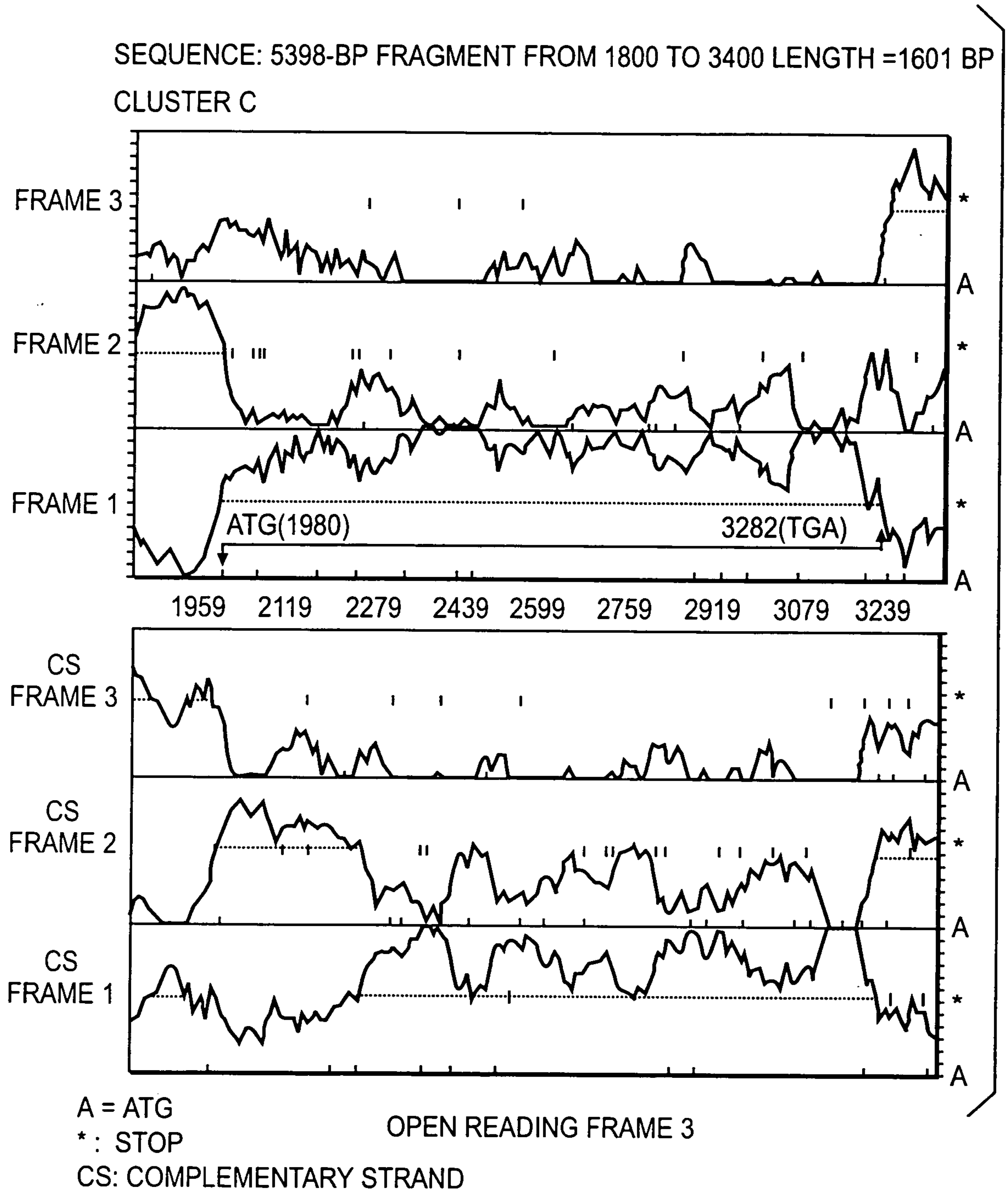

SEQUENCE: 5398-BP FRAGMENT FROM 1000 TO 2200 LENGTH =1201 BP
FRAME 3
FRAME 2
FRAME 1
ATG(1141)
TGA(1981)
1119 1239 1359 1479 1599 1719 1839 1959 2879
CS FRAME 3
CS FRAME 2
CS FRAME 1
A
*
A = ATG
* : STOP
CS: COMPLEMENTARY STRAND
OPEN READING FRAME 2

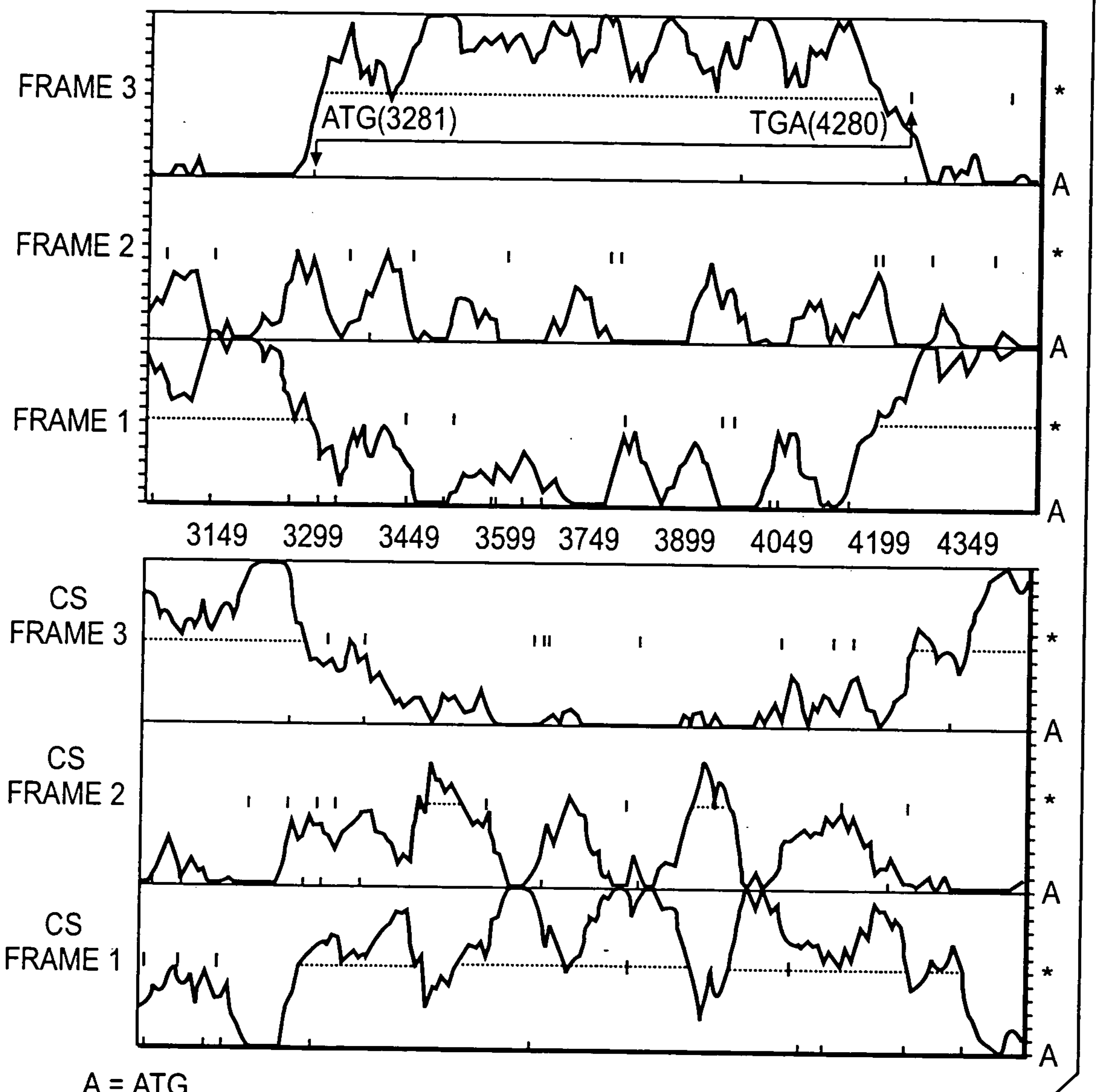
FIG. 9B



OPEN READING FRAME 3

FIG. 9C

SEQUENCE: 5398-BP FRAGMENT FROM 3000 TO 4500 LENGTH =1501 BP
CLUSTER C



A = ATG
* : STOP
CS: COMPLEMENTARY STRAND

OPEN READING FRAME 4

FIG. 9D

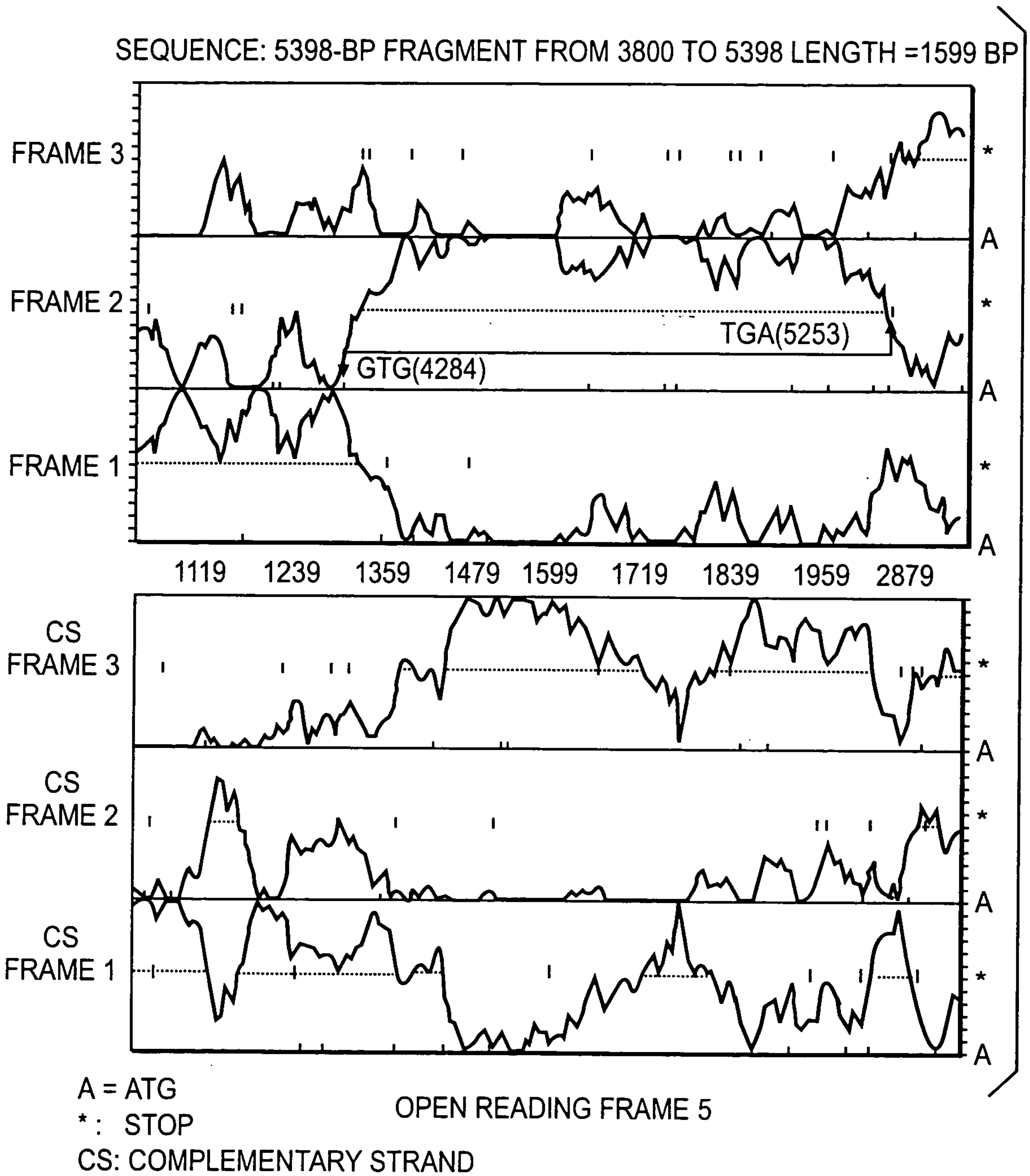
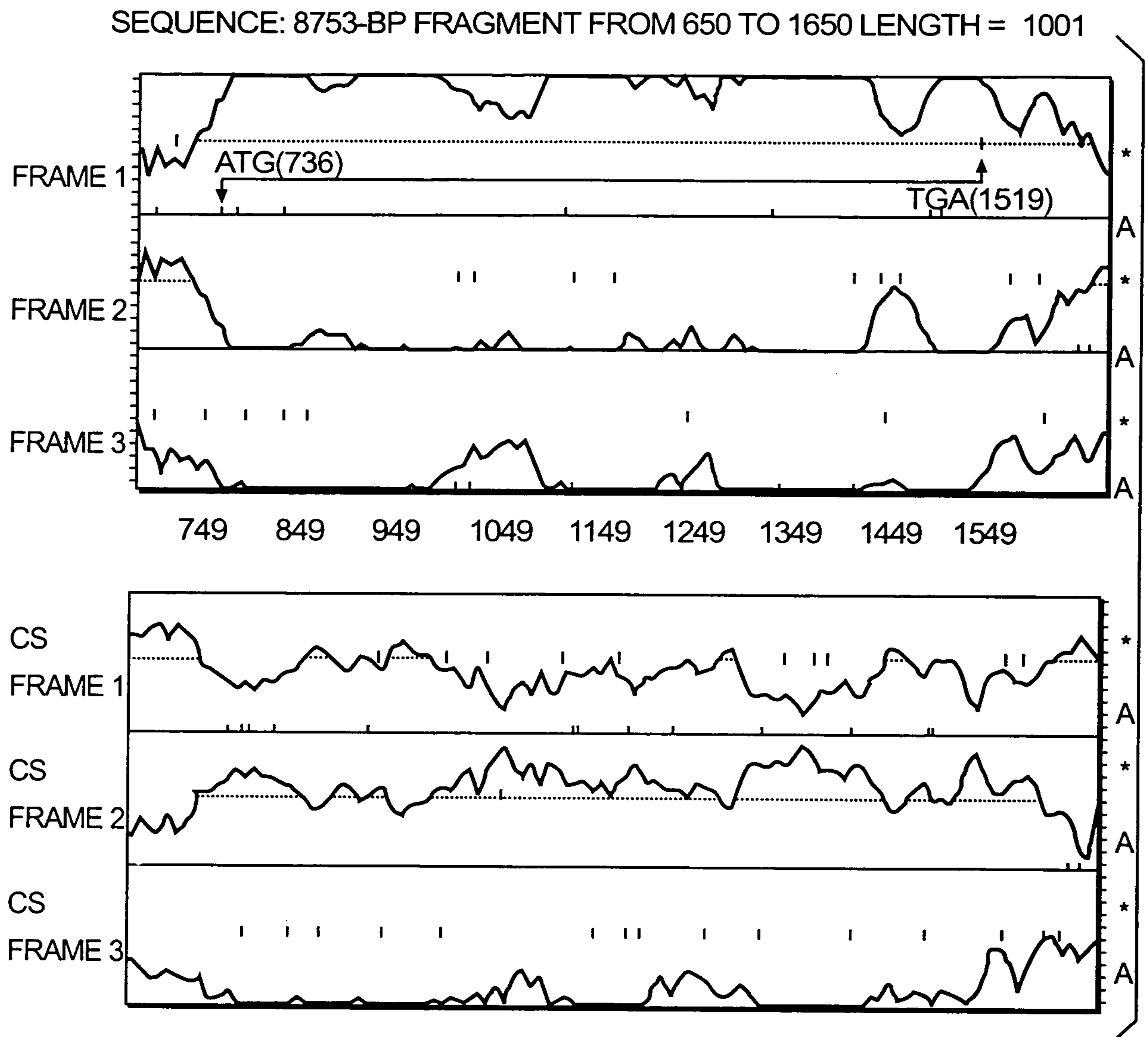

SEQUENCE: 5398-BP FRAGMENT FROM 3800 TO 5398 LENGTH =1599 BP
FRAME 3
FRAME 2
FRAME 1
TGA(5253)
GTG(4284)
A
*
1119 1239 1359 1479 1599 1719 1839 1959 2879
CS FRAME 3
CS FRAME 2
CS FRAME 1
A = ATG
*: STOP
CS: COMPLEMENTARY STRAND
OPEN READING FRAME 5

FIG. 9E



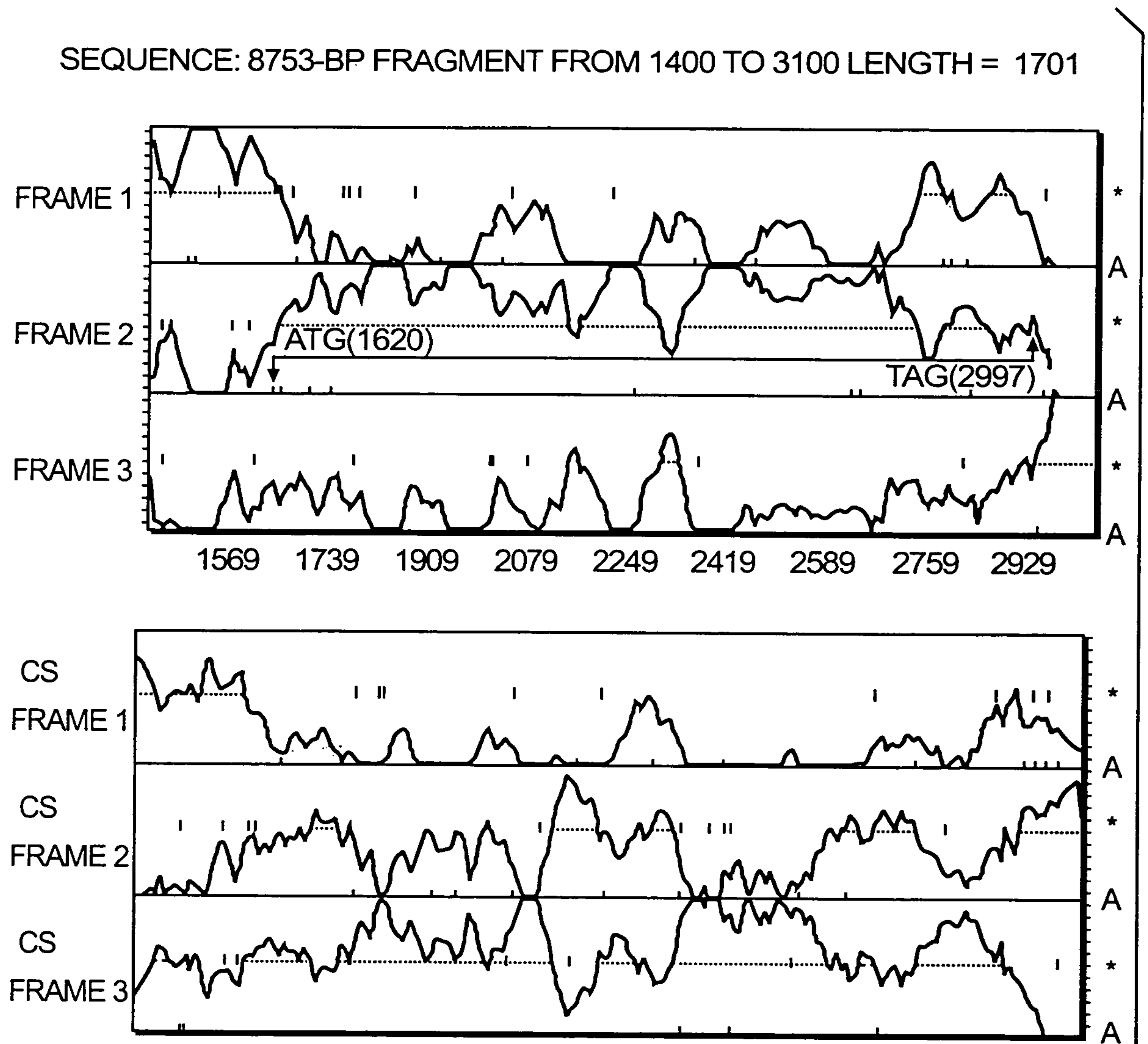
OPEN READING FRAME 6

A = ATG

*: STOP

CS: COMPLEMENTARY STRAND

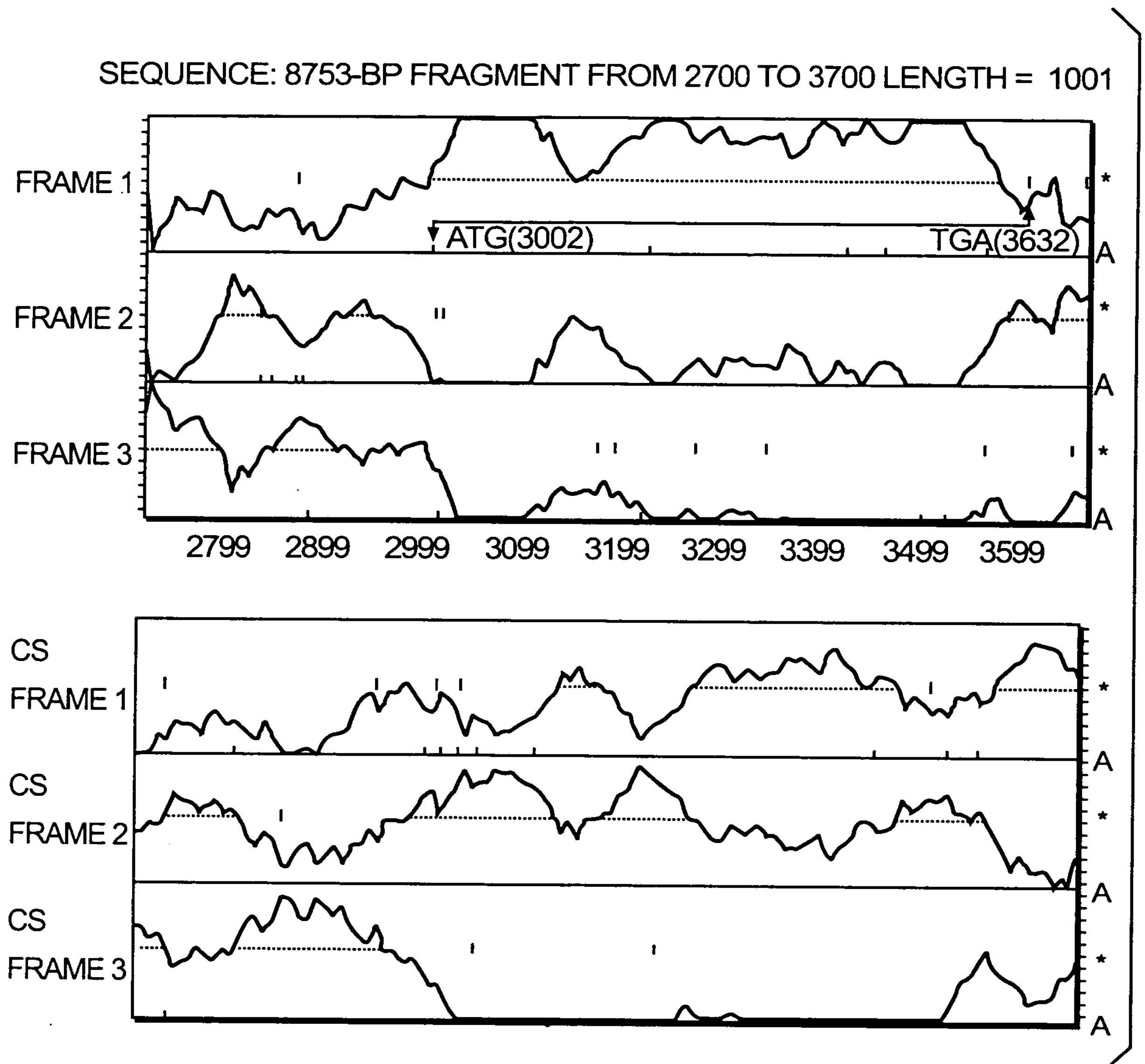
FIG. 10A



OPEN READING FRAME 7

A = ATG
*: STOP
CS: COMPLEMENTARY STRAND

FIG. 10B



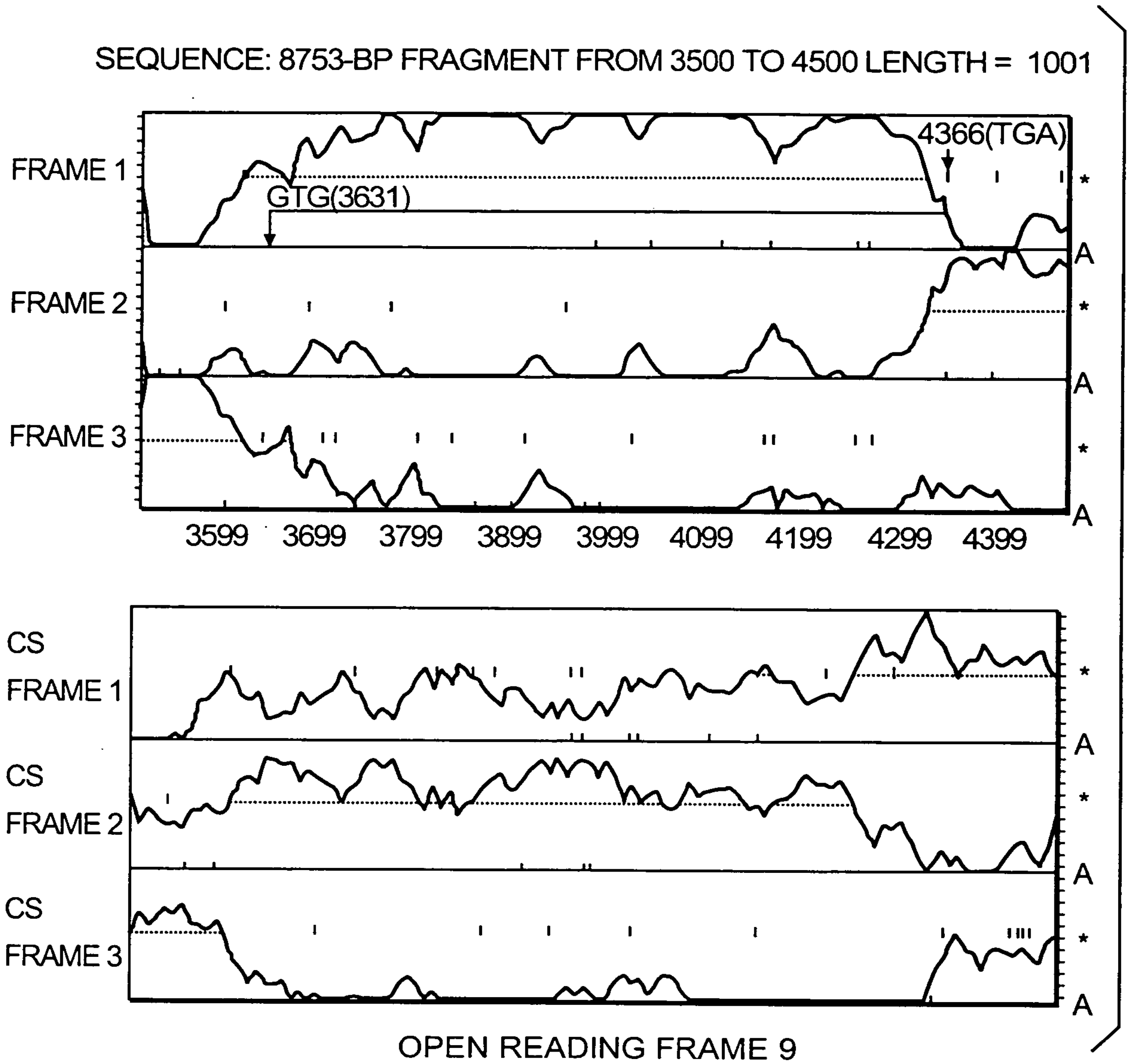
OPEN READING FRAME 8

A = ATG

*: STOP

CS: COMPLEMENTARY STRAND

FIG. 10C



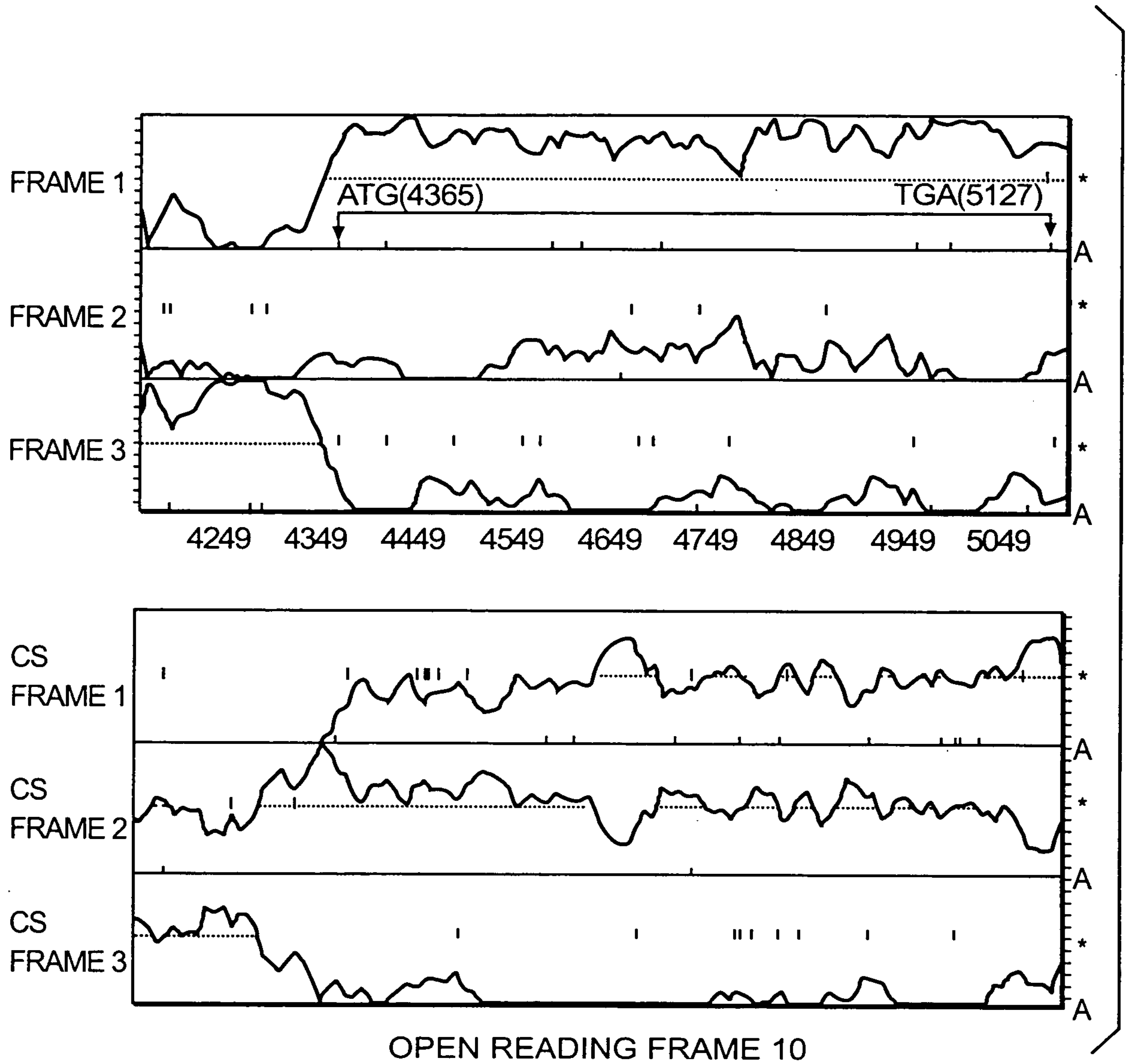
A = ATG

*: STOP

CS: COMPLEMENTARY STRAND

FIG. 10D

SEQUENCE: 8753-BP FRAGMENT FROM 4150 TO 5150 LENGTH = 1001



OPEN READING FRAME 10

A = ATG

*: STOP

CS: COMPLEMENTARY STRAND

FIG. 10E

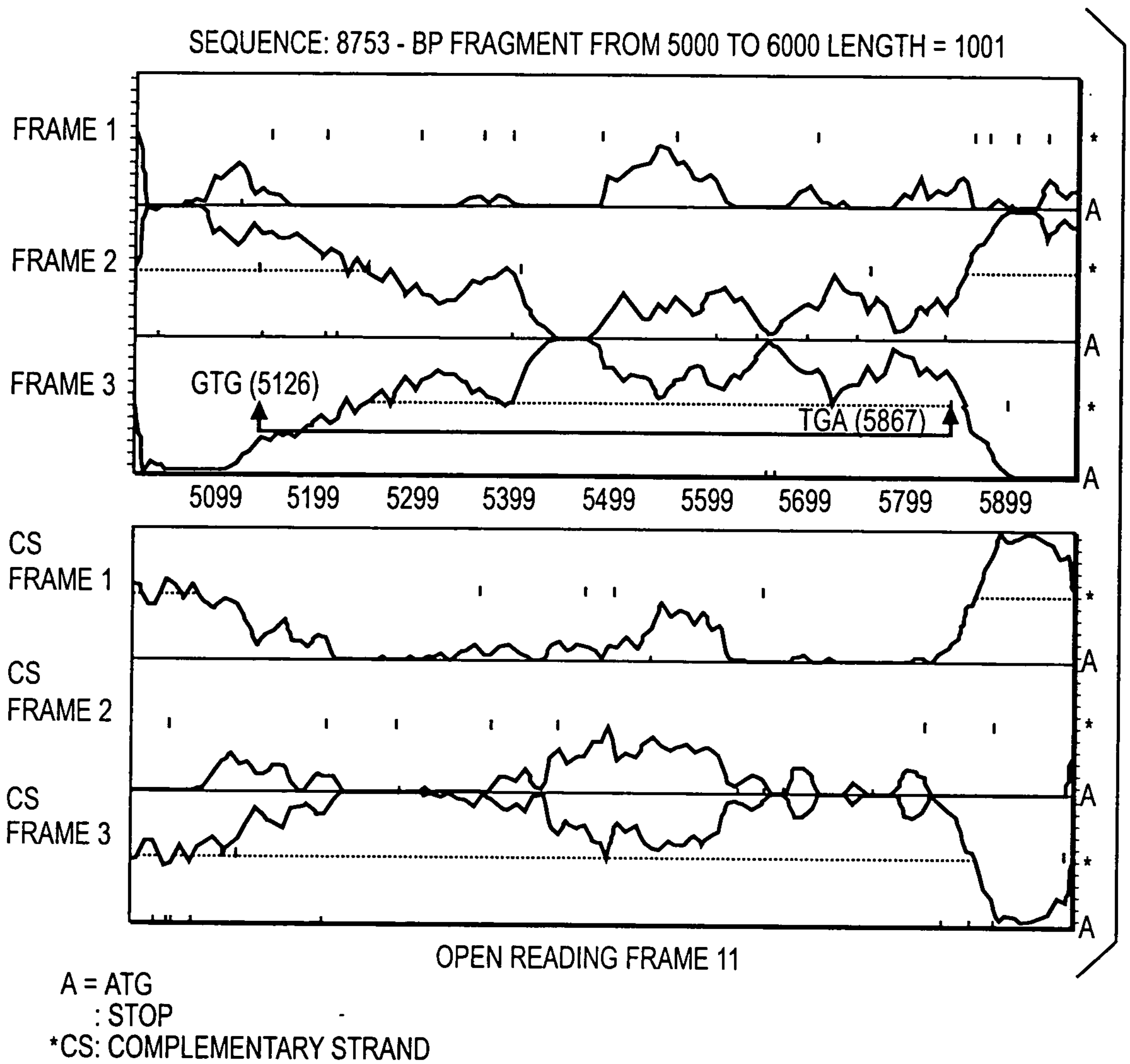
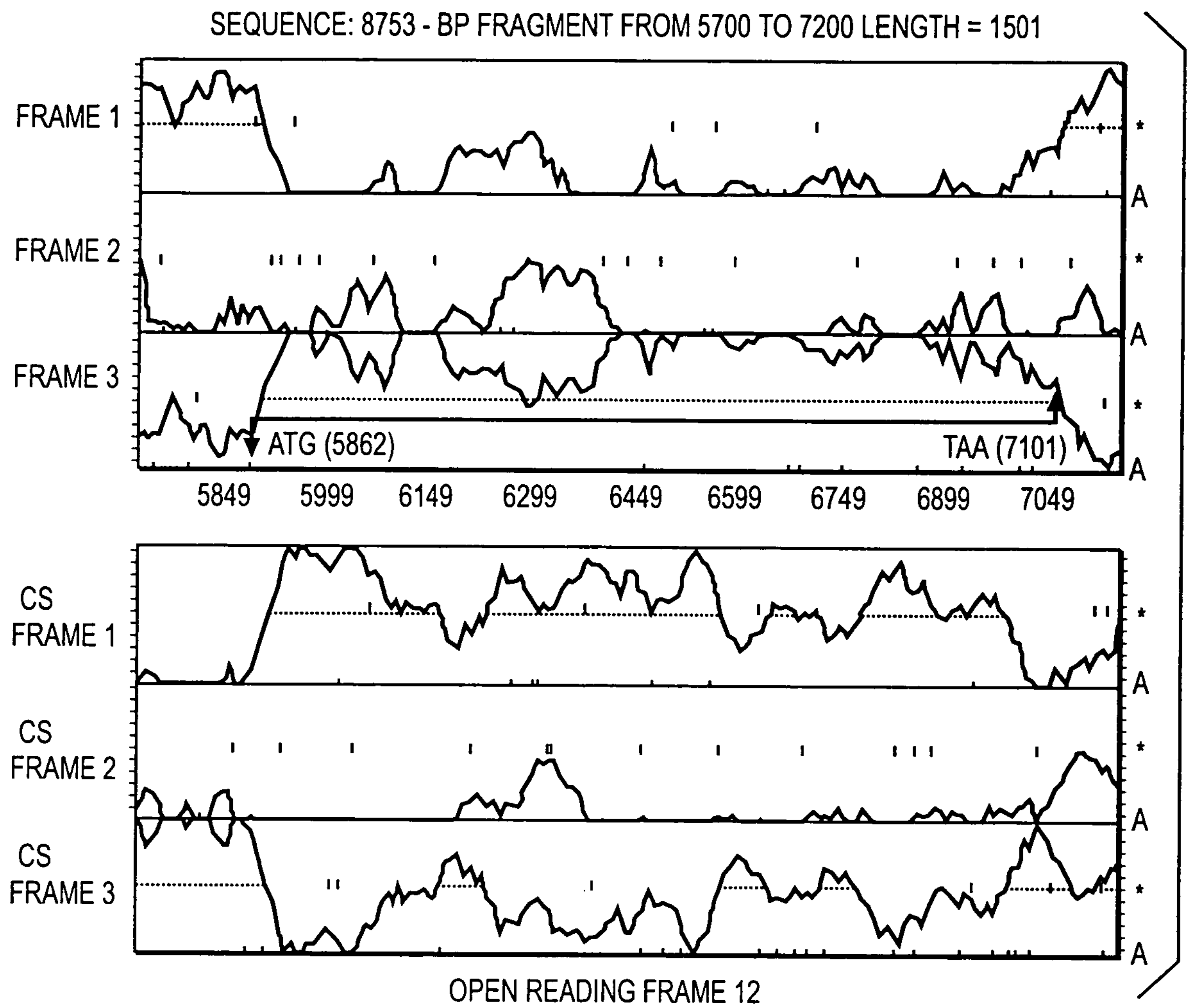
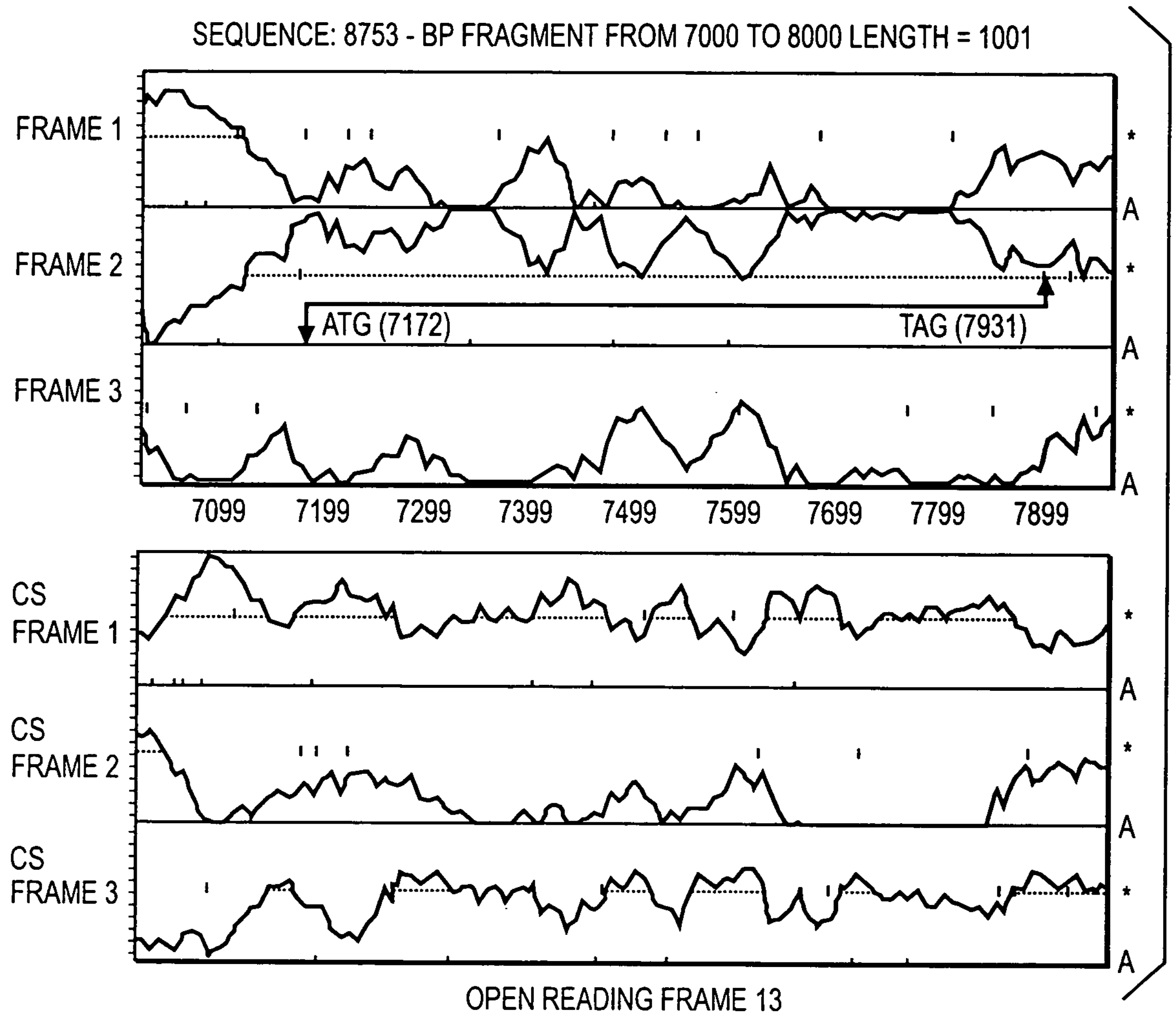

SEQUENCE: 8753 - BP FRAGMENT FROM 5000 TO 6000 LENGTH = 1001
FRAME 1
FRAME 2
FRAME 3
GTG (5126)
TGA (5867)
5099
5199
5299
5399
5499
5599
5699
5799
5899
CS FRAME 1
CS FRAME 2
CS FRAME 3
A
*
OPEN READING FRAME 11
A = ATG
: STOP
*CS: COMPLEMENTARY STRAND

FIG. 10F



A = ATG
: STOP
* CS: COMPLEMENTARY STRAND

FIG. 10G



OPEN READING FRAME 13

A = ATG
* : STOP
CS: COMPLEMENTARY STRAND

FIG. 10H

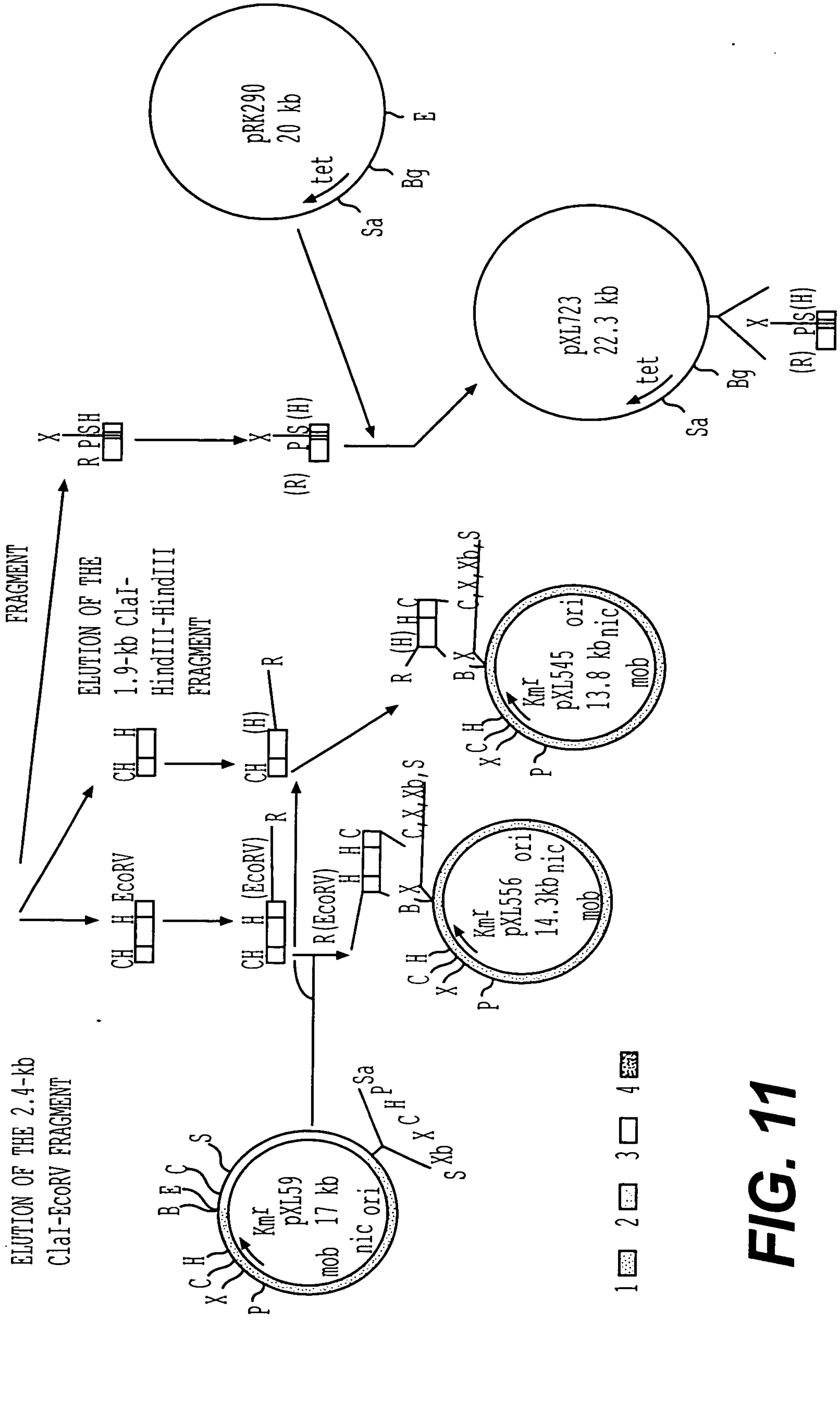
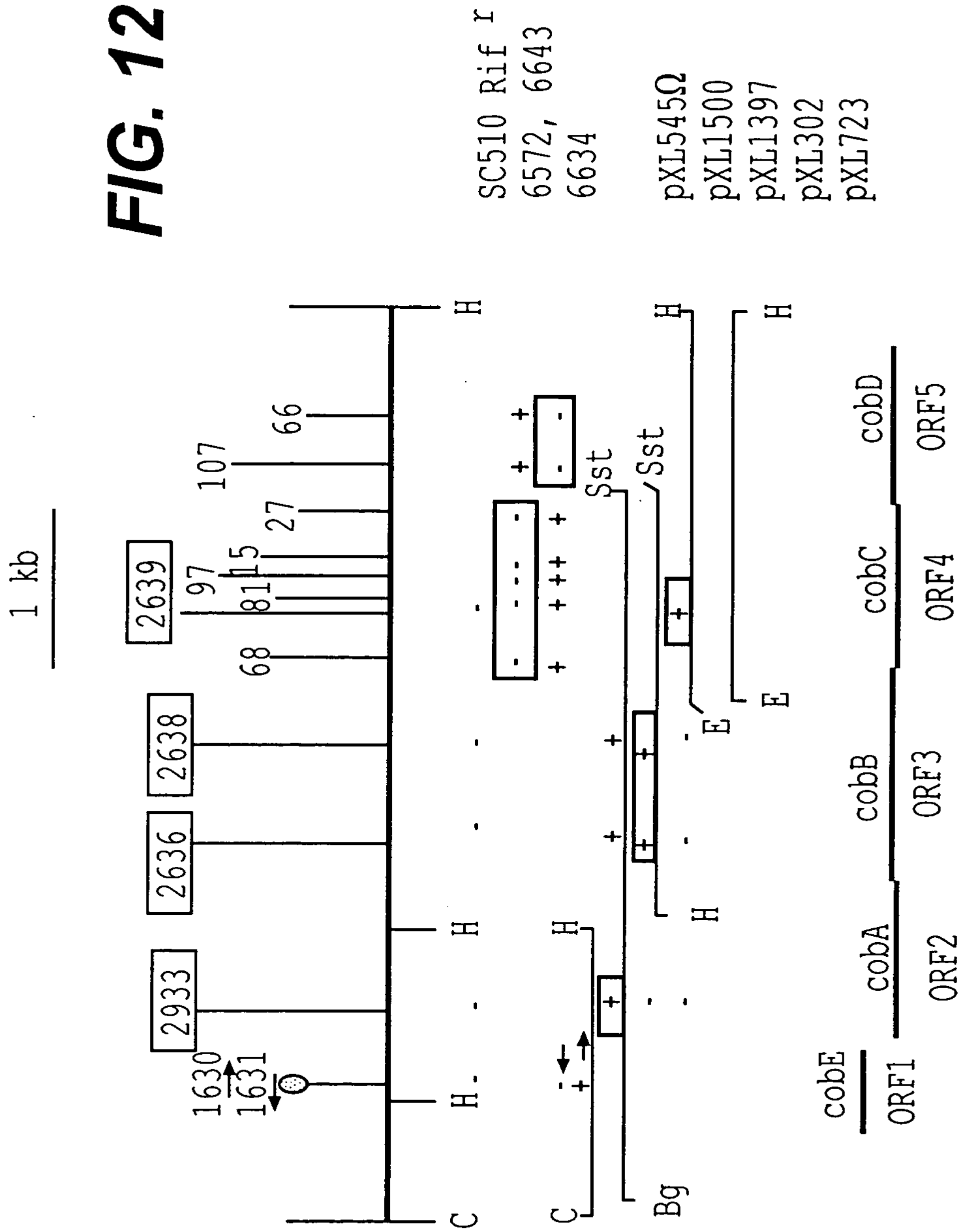

ELUTION OF THE 2.4-kb ClaI-EcoRV FRAGMENT
ELUTION OF THE 2.3-kb EcoRI-HindIII FRAGMENT
ELUTION OF THE 1.9-kb ClaI-HindIII-HindIII FRAGMENT
pXL59 17 kb
Km^r
mob
nic ori
pXL556 14.3kb
pXL545 13.8 kb
pRK290 20 kb
pXL723 22.3 kb
tet
Sa
Bg
E
1
2
3
4

FIG. 11

FIG. 12


1 kb
2933
2636
2638
2639
1630
1631
68
81
97
15
27
107
66
C
H
H
H
C
H
Bg
Sst
Sst
H
E
H
E
H
SC510 Rif r
6572, 6643
6634
pXL545Ω
pXL1500
pXL1397
pXL302
pXL723
cobE
cobA
cobB
cobC
cobD
ORF1
ORF2
ORF3
ORF4
ORF5

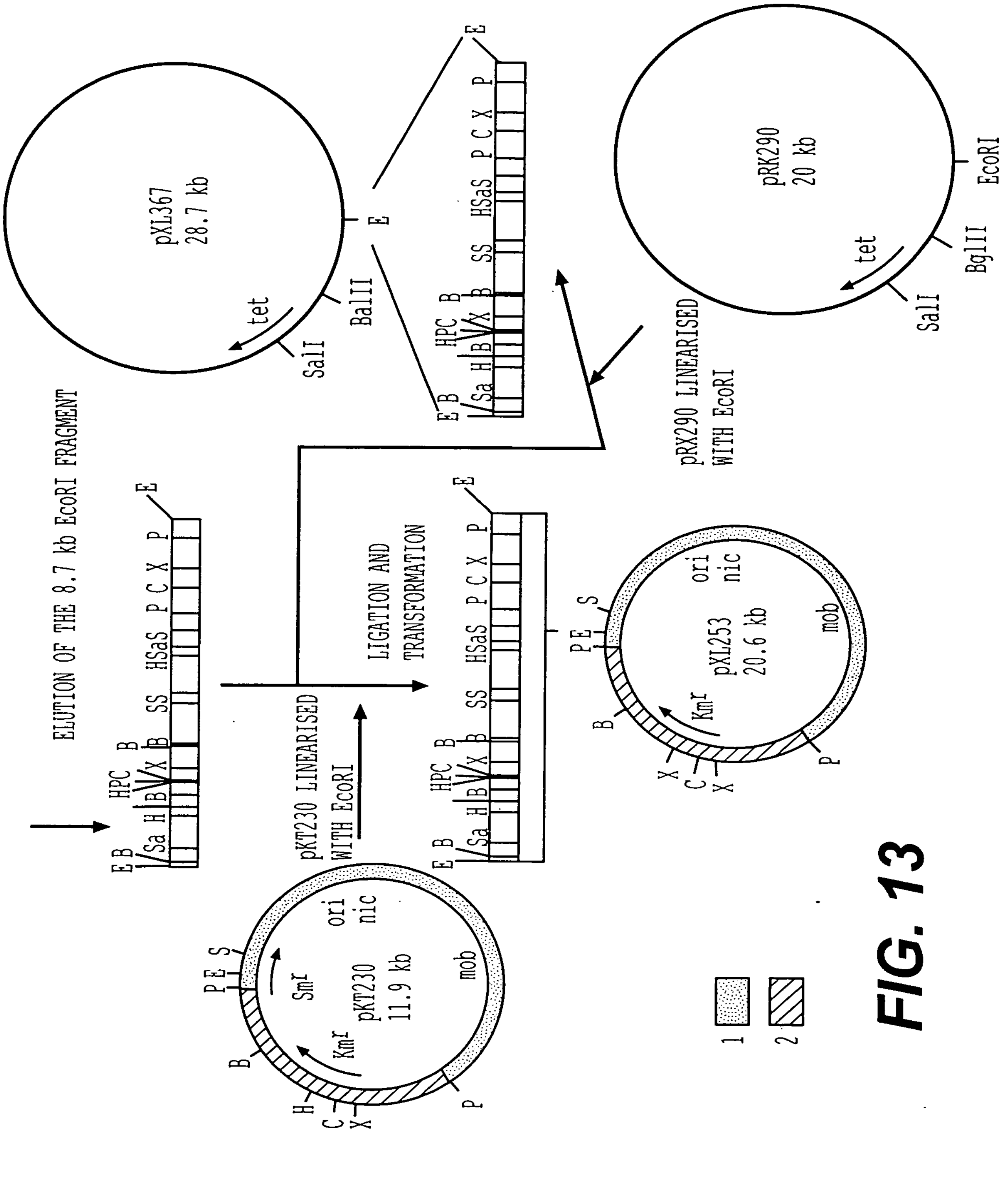

pXL367
28.7 kb
tet
SalI
BalII
E
E B
Sa H B
HPC B
X B
SS
HSaS
P C X
P
E
pRK290
20 kb
tet
SalI
BglII
EcoRI
pRX290 LINEARISED
WITH EcoRI
ELUTION OF THE 8.7 kb EcoRI FRAGMENT
pKT230 LINEARISED
WITH EcoRI
LIGATION AND
TRANSFORMATION
pKT230
11.9 kb
Sm^r
Km^r
ori
nic
mob
P E S
B
H
C
X
P
pXL253
20.6 kb
Km^r
ori
nic
mob
P E S
B
X
C
X
P
1
2

FIG. 13

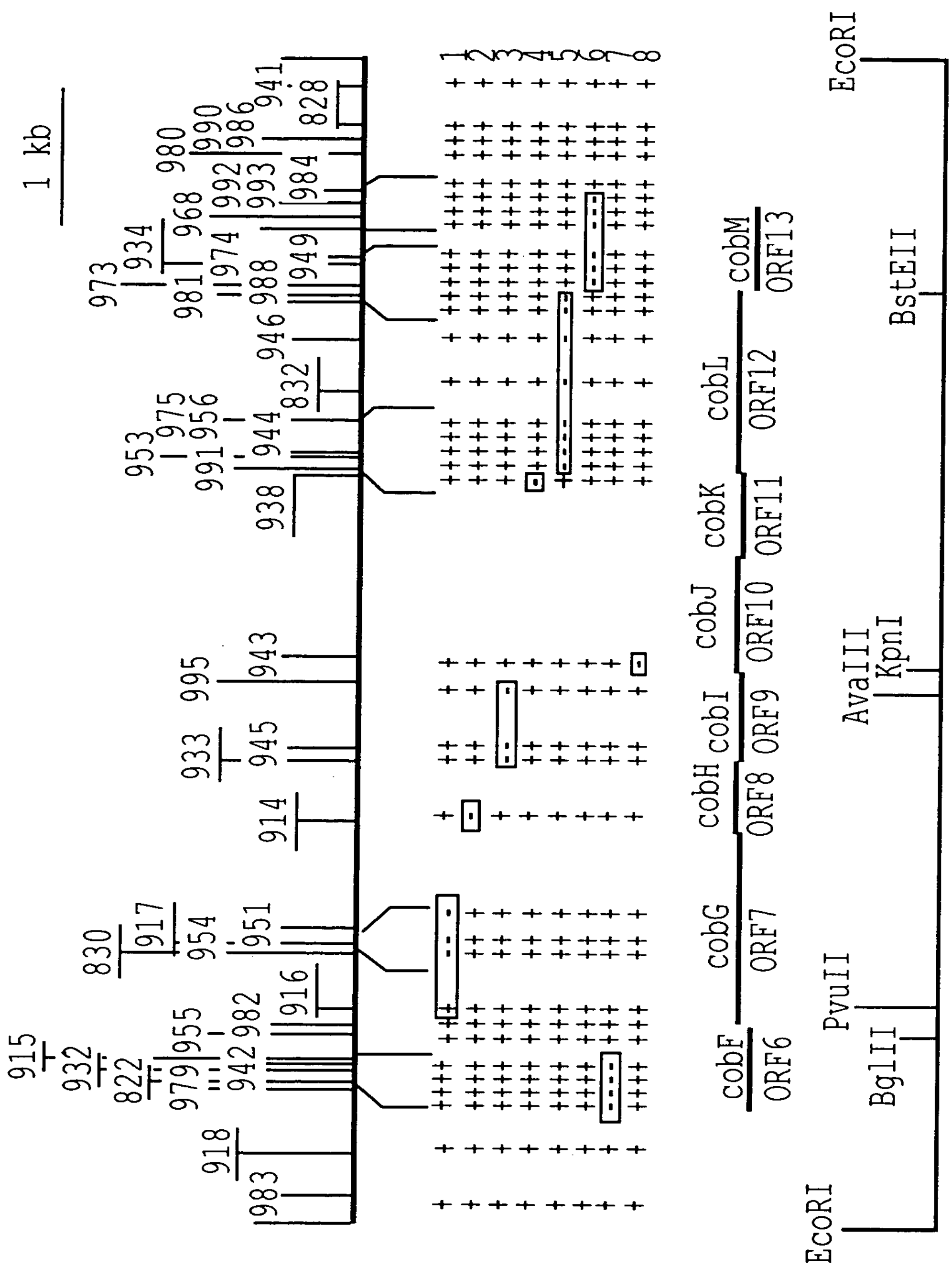

1 kb
EcoRI
BglII
PvuII
AvaIII
KpnI
BstEII
EcoRI
cobF
ORF6
cobG
ORF7
cobH
ORF8
cobI
ORF9
cobJ
ORF10
cobK
ORF11
cobL
ORF12
cobM
ORF13
983
918
979
822
932
915
942
955
982
916
830
917
954
951
914
933
945
995
943
938
991
953
944
975
956
832
946
981
973
934
988
974
968
949
992
993
984
980
990
986
828
941
1
2
3
4
5
6
7
8

FIG. 14

cobA GENE (SEQ ID NO: 3) AND COBA PROTEIN (SEQ ID NO: 4)
SEQUENCE OF THE 5396-BP ClaI-HindIII-HindIII-HindIII FRAGMENT
FROM 1141 TO 1980

```
MetIleAspAspLeuPheAlaGlyLeuProAlaLeuGluLysGlySerValTrpLeuValGlyAlaGlyProGly
ATGATCGACGACCTCTTTGCCGGATTGCCGGCGCTCGAAAAAGGTTCGGTCTGGCTGGTCGGCGCCGGCCCCGGC
    1141      1151      1161      1171      1181      1191      1201
AspProGlyLeuLeuThrLeuHisAlaAlaAsnAlaLeuArgGlnAlaAspValIleValHisAspAlaLeuVal
GATCCCGGCCTGTTGACGCTGCATGCGGCCAATGCGCTGCGCCAGGCGGATGTGATCGTGCATGATGCGCTGGTC
    1216      1226      1236      1246      1256      1266      1276
AsnGluAspCysLeuLysLeuAlaArgProGlyAlaValLeuGluPheAlaGlyLysArgGlyGlyLysProSer
AACGAGGATTGCCTGAAGCTCGCGCGGCCGGGCGCCGTGCTGGAGTTTGCGGGCAAGCGTGGCGGCAAGCCGTCG
    1291      1301      1311      1321      1331      1341      1351
ProLysGlnArgAspIleSerLeuArgLeuValGluLeuAlaArgAlaGlyAsnArgValLeuArgLeuLysGly
CCGAAGCAGCGCGACATCTCGCTTCGCCTCGTCGAACTCGCGCGCGCCGGCAACCGGGTGCTGCGCCTCAAAGGC
    1366      1376      1386      1396      1406      1416      1426
GlyAspProPheValPheGlyArgGlyGlyGluGluAlaLeuThrLeuValGluHisGlnValProPheArgIle
GGCGATCCCTTCGTCTTCGGTCGCGGTGGCGAGGAGGCGCTGACGCTGGTCGAACACCAGGTGCCGTTCCGAATC
    1441      1451      1461      1471      1481      1491      1501
ValProGlyIleThrAlaGlyIleGlyGlyLeuAlaTyrAlaGlyIleProValThrHisArgGluValAsnHis
GTGCCCGGCATCACCGCCGGTATCGGCGGGCTTGCCTATGCCGGCATTCCCGTGACCCATCGCGAGGTCAACCAC
    1516      1526      1536      1546      1556      1566      1576
AlaValThrPheLeuThrGlyHisAspSerSerGlyLeuValProAspArgIleAsnTrpGlnGlyIleAlaSer
GCGGTCACTTTCCTGACTGGCCATGATTCCTCCGGCCTGGTGCCGGATCGCATCAACTGGCAGGGCATCGCCAGC
    1591      1601      1611      1621      1631      1641      1651
GlySerProValIleValMetTyrMetAlaMetLysHisIleGlyAlaIleThrAlaAsnLeuIleAlaGlyGly
GGCTCGCCTGTCATCGTCATGTACATGGCGATGAAACATATCGGCGCGATCACCGCCAACCTCATTGCCGGCGGC
    1666      1676      1686      1696      1706      1716      1726
ArgSerProAspGluProValAlaPheValCysAsnAlaAlaThrProGlnGlnAlaValLeuGluThrThrLeu
CGCTCGCCGGACGAACCGGTCGCCTTCGTCTGCAACGCCGCGACGCCGCAGCAGGCGGTGCTGGAAACGACGCTT
    1741      1751      1761      1771      1781      1791      1801
AlaArgAlaGluAlaAspValAlaAlaAlaGlyLeuGluProProAlaIleValValValGlyGluValValArg
GCGCGTGCAGAGGCCGATGTTGCGGCGGCAGGGCTGGAGCCGCCGGCGATCGTCGTCGTCGGCGAGGTGGTGCGG
    1816      1826      1836      1846      1856      1866      1876
LeuArgAlaAlaLeuAspTrpIleGlyAlaLeuAspGlyArgLysLeuAlaAlaAspProPheAlaAsnArgIle
CTGCGCGCAGCGCTCGACTGGATCGGCGCGCTGGACGGGCGCAAGCTTGCCGCCGACCCGTTCGCCAATCGCATT
    1891      1901      1911      1921      1931      1941      1951
                              LeuArgAsnProAla***
                              CTCAGGAACCCGGCATGA
    1966      1976      1986      1996      2006      2016      2026
```

FIG. 15A

NAME = COBA

FIRST RESIDUE = 1
LAST RESIDUE = 280

			NUMBER	NO. %	WEIGHT	WEIGHT %
1	PHE	F	8	2.86	1176.56	4.02
2	LEU	L	31	11.07	3505.48	11.99
3	ILE	I	16	5.71	1809.28	6.19
4	MET	M	4	1.43	524.16	1.79
5	VAL	V	27	9.64	2674.89	9.15
6	SER	S	8	2.86	696.24	2.38
7	PRO	P	19	6.79	1843.95	6.31
8	THR	T	10	3.57	1010.50	3.46
9	ALA	A	41	14.64	2912.64	9.96
10	TYR	Y	2	0.71	326.12	1.12
11	*	*	0	0.00	0.00	0.00
12	HIS	H	7	2.50	959.42	3.28
13	GLN	Q	6	2.14	768.36	2.63
14	ASN	N	9	3.21	1026.36	3.51
15	LYS	K	8	2.86	1024.72	3.51
16	ASP	D	15	5.36	1725.45	5.90
17	GLU	E	13	4.64	1677.52	5.74
18	CYS	C	2	0.71	206.02	0.70
19	TRP	W	3	1.07	558.24	1.91
20	ARG	R	19	6.79	2965.90	10.15
21	GLY	G	32	11.43	1824.64	6.24
22	-	-	0	0.00	0.00	0.00

RESIDUES = 280
MOLECULAR WEIGHT = 29234.
INDEX OF POLARITY (%) = 34.
ISOELECTRIC POINT = 7.51
OD 260 (1mg/ml) = 0.464 OD 280 (1mg/ml) = 0.652

HYDROPHILICITY PROFILE OF THE COBA PROTEIN
COBA FROM 1 TO 280

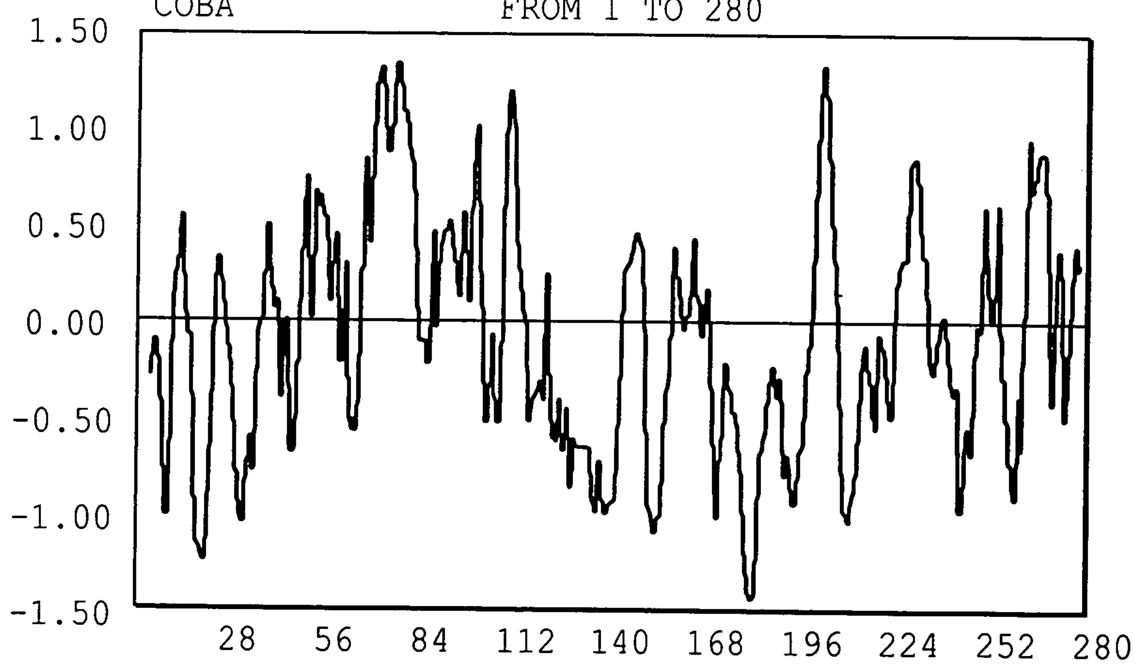


FIG. 15B

cobB GENE (SEQ ID NO: 5) AND COBB PROTEIN (SEQ ID NO: 6)
SEQUENCE OF THE 5396-BP ClaI-HindIII-HindIII-HindIII FRAGMENT
FROM 1980 TO 3281

```
   MetSerGlyLeuLeuIleAlaAlaProAlaSerGlySerGlyLysThrThrValThrLeuGlyLeuMetArgAla
   ATGAGCGGATTGCTGATTGCCGCACCCGCGTCCGGCTCCGGCAAGACGACGGTGACGCTCGGGCTGATGCGCGCC
1980      1990      2000      2010      2020      2030      2040
   LeuLysArgArgGlyValAlaIleAlaProGlyLysAlaGlyProAspTyrIleAspProAlaPheHisAlaAla
   CTGAAGAGGCGCGGCGTGGCGATCGCGCCCGGCAAGGCGGGGCCGGACTATATCGATCCCGCTTTCCACGCGGCA
2055      2065      2075      2085      2095      2105      2115
   AlaThrGlyGluProCysPheAsnTyrAspProTrpAlaMetArgProGluLeuLeuLeuAlaAsnAlaSerHis
   GCGACCGGCGAGCCCTGCTTCAACTACGACCCCTGGGCGATGCGCCCGGAACTGCTGCTTGCCAATGCGTCGCAT
2130      2140      2150      2160      2170      2180      2190
   ValAlaSerGlyGlyArgThrLeuIleValGluAlaMetMetGlyLeuHisAspGlyAlaAlaAspGlySerGly
   GTGGCCTCCGGCGGGCGCACATTGATCGTCGAGGCGATGATGGGACTGCATGACGGTGCTGCCGACGGCTCGGGA
2205      2215      2225      2235      2245      2255      2265
   ThrProAlaAspLeuAlaAlaThrLeuAsnLeuAlaValIleLeuValValAspCysAlaArgMetSerGlnSer
   ACGCCAGCGGACCTCGCCGCGACGCTGAACCTTGCGGTCATTCTGGTGGTCGATTGCGCCCGCATGTCCCAGTCG
2280      2290      2300      2310      2320      2330      2340
   ValAlaAlaLeuValArgGlyTyrAlaAspHisArgAspAspIleArgValValGlyValIleLeuAsnLysVal
   GTTGCCGCCCTCGTGCGCGGCTATGCGGATCATCGCGACGATATCCGGGTGGTTGGCGTCATCCTCAACAAGGTC
2355      2365      2375      2385      2395      2405      2415
   GlySerAspArgHisGluMetMetLeuArgAspAlaLeuGlyLysValArgMetProValPheGlyValLeuArg
   GGCAGCGATCGGCATGAAATGATGCTGCGCGATGCGCTCGGCAAGGTGCGCATGCCTGTCTTCGGCGTGCTCCGG
2430      2440      2450      2460      2470      2480      2490
   GlnAspSerAlaLeuGlnLeuProGluArgHisLeuGlyLeuValGlnAlaGlyGluHisSerAlaLeuGluGly
   CAGGACAGCGCATTGCAACTGCCGGAGCGCCATCTCGGGCTCGTGCAGGCGGGCGAACACTCAGCGCTTGAGGGC
2505      2515      2525      2535      2545      2555      2565
   PheIleGluAlaAlaAlaAlaArgValGluAlaAlaCysAspLeuAspAlaIleArgLeuIleAlaThrIlePhe
   TTCATCGAGGCGGCGGCCGCGCGGGTCGAGGCTGCCTGCGATCTCGACGCCATCCGCCTGATCGCGACGATTTTC
2580      2590      2600      2610      2620      2630      2640
   ProGlnValProAlaAlaAlaAspAlaGluArgLeuArgProLeuGlyGlnArgIleAlaValAlaArgAspIle
   CCGCAGGTGCCCGCGGCGGCCGATGCCGAGCGTTTGCGGCCGCTCGGTCAGCGCATCGCGGTCGCGCGCGATATC
2655      2665      2675      2685      2695      2705      2715
   AlaPheAlaPheCysTyrGluHisLeuLeuTyrGlyTrpArgGlnGlyGlyAlaGluIleSerPhePheSerPro
   GCCTTTGCCTTCTGCTACGAGCACCTGCTTTACGGCTGGCGGCAAGGCGGCGCGGAGATTTCCTTCTTCTCGCCG
2730      2740      2750      2760      2770      2780      2790
   LeuAlaAspGluGlyProAspAlaAlaAlaAspAlaValTyrLeuProGlyGlyTyrProGluLeuHisAlaGly
   CTCGCCGACGAGGGGCCGGATGCGGCAGCCGATGCCGTCTATCTTCCGGGGGGTTATCCGGAGCTGCATGCGGGG
2805      2815      2825      2835      2845      2855      2865
```

FIG. 15C

```
 GlnLeuSerAlaAlaAlaArgPheArgSerGlyMetHisSerAlaAlaGluArgGlyAlaArgIlePheGlyGlu
 CAGCTGAGCGCCGCCGCCCGATTCCGTTCCGGCATGCATTCCGCGGCGGAACGCGGCGCCCGCATCTTCGGCGAG
2880      2890      2900      2910      2920      2930      2940
 CysGlyGlyTyrMetValLeuGlyGluGlyLeuValAlaAlaAspGlyThrArgTyrAspMetLeuGlyLeuLeu
 TGCGGCGGCTATATGGTGCTCGGCGAAGGGCTTGTCGCTGCCGATGGCACACGCTACGACATGCTCGGCCTGCTG
2955      2965      2975      2985      2995      3005      3015
 ProLeuValThrSerPheAlaGluArgArgArgHisLeuGlyTyrArgArgValValProValAspAsnAlaPhe
 CCGCTCGTAACCAGTTTTGCCGAGCGCAGGCGGCACCTCGGCTATCGCCGCGTCGTGCCTGTCGACAACGCCTTC
3030      3040      3050      3060      3070      3080      3090
 PheAspGlyProMetThrAlaHisGluPheHisTyrAlaThrIleValAlaGluGlyAlaAlaAspArgLeuPhe
 TTCGATGGACCCATGACGGCGCACGAATTCCACTATGCGACCATCGTCGCCGAAGGGGCGGCCGATCGGCTGTTT
3105      3115      3125      3135      3145      3155      3165
 AlaValSerAspAlaAlaGlyGluAspLeuGlyGlnAlaGlyLeuArgArgGlyProValAlaGlySerPheMet
 GCGGTCAGCGACGCCGCCGGCGAGGATCTCGGCCAGGCGGGCCTCCGGCGCGGCCCTGTCGCCGGTTCCTTCATG
3180      3190      3200      3210      3220      3230      3240
 HisLeuIleAspValAlaGlyAlaAla***
 CATCTGATCGACGTCGCAGGTGCTGCATGA
3255      3265      3275      3285      3295      3305      3315
```

FIG. 15D

NAME = COBB

FIRST RESIDUE = 1
LAST RESIDUE = 434

			NUMBER	NO. %	WEIGHT	WEIGHT %
1	PHE	F	17	3.92	2500.19	5.47
2	LEU	L	45	10.37	5088.60	11.14
3	ILE	I	17	3.92	1922.36	4.21
4	MET	M	14	3.23	1834.56	4.02
5	VAL	V	31	7.14	3071.17	6.72
6	SER	S	19	4.38	1653.57	3.62
7	PRO	P	21	4.84	2038.05	4.46
8	THR	T	12	2.76	1212.60	2.65
9	ALA	A	76	17.51	5399.04	11.82
10	TYR	Y	11	2.53	1793.66	3.93
11	*	*	0	0.00	0.00	0.00
12	HIS	H	14	3.23	1918.84	4.20
13	GLN	Q	9	2.07	1152.54	2.52
14	ASN	N	5	1.15	570.20	1.25
15	LYS	K	5	1.15	640.45	1.40
16	ASP	D	28	6.45	3220.84	7.05
17	GLU	E	21	4.84	2709.84	5.93
18	CYS	C	5	1.15	515.05	1.13
19	TRP	W	2	0.46	372.16	0.81
20	ARG	R	34	7.83	5307.40	11.62
21	GLY	G	48	11.06	2736.96	5.99
22	-	-	0	0.00	0.00	0.00

RESIDUES = 434
MOLECULAR WEIGHT = 45676.
INDEX OF POLARITY (%) = 34.
ISOELECTRIC POINT = 6.47
OD 260 (1mg/ml) = 0.351 OD 280 (1mg/ml) = 0.529

HYDROPHILICITY PROFILE OF THE COBB PROTEIN

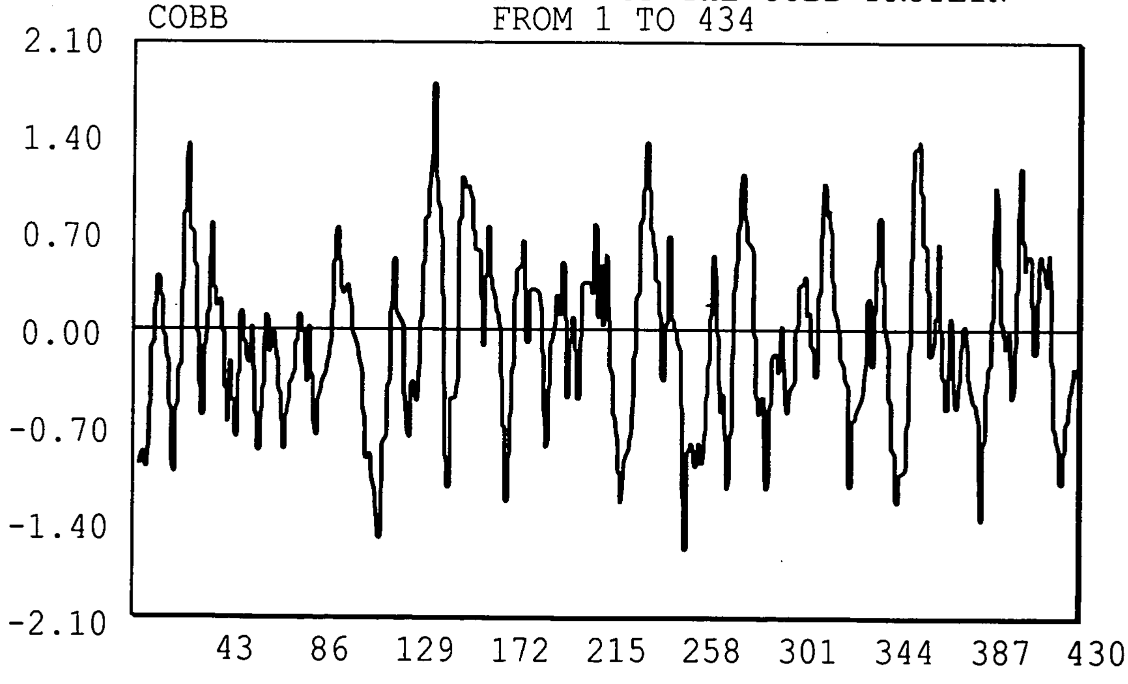


FIG. 15E

cobC GENE (SEQ ID NO: 7) AND COBC PROTEIN (SEQ ID NO: 8)
SEQUENCE OF THE 5396-BP ClaI-HindIII-HindIII-HindIII FRAGMENT
FROM 3281 TO 4279

```
    MetSerAlaProIleValHisGlyGlyGlyIleThrGluAlaAlaAlaArgTyrGlyGlyArgProGluAspTrp
    ATGAGCGCACCGATCGTTCATGGTGGCGGCATCACCGAGGCCGCAGCGCGCTATGGCGGCCGGCCTGAAGACTGG
3281      3291      3301      3311      3321      3331      3341
    LeuAspLeuSerThrGlyIleAsnProCysProValAlaLeuProAlaValProGluArgAlaTrpHisArgLeu
    CTCGATCTGTCGACCGGCATCAATCCATGCCCCGTCGCCTTGCCCGCGGTCCCTGAGCGCGCCTGGCACCGGCTG
3356      3366      3376      3386      3396      3406      3416
    ProAspArgGlnThrValAspAspAlaArgSerAlaAlaAlaAspTyrTyrArgThrAsnGlyValLeuProLeu
    CCGGATCGGCAGACGGTAGATGATGCGCGGAGCGCCGCCGCCGACTACTACCGCACCAACGGCGTGCTGCCTTTG
3431      3441      3451      3461      3471      3481      3491
    ProValProGlyThrGlnSerValIleGlnLeuLeuProArgLeuAlaProAlaAsnArgHisValAlaIlePhe
    CCGGTGCCGGGCACCCAGTCGGTGATCCAGCTCCTGCCACGTCTTGCTCCGGCCAACAGGCACGTCGCGATTTTC
3506      3516      3526      3536      3546      3556      3566
    GlyProThrTyrGlyGluTyrAlaArgValLeuGluAlaAlaGlyPheAlaValAspArgValAlaAspAlaAsp
    GGGCCGACCTATGGCGAGTATGCCCGCGTGCTTGAAGCGGCCGGCTTTGCTGTCGATCGCGTCGCGGATGCCGAC
3581      3591      3601      3611      3621      3631      3641
    AlaLeuThrAlaGluHisGlyLeuValIleValValAsnProAsnAsnProThrGlyArgAlaLeuAlaProAla
    GCGCTCACGGCCGAACATGGGCTTGTCATCGTCGTCAACCCCAACAACCCGACCGGCCGCGCCTTGGCGCCGGCG
3656      3666      3676      3686      3696      3706      3716
    GluLeuLeuAlaIleAlaAlaArgGlnLysAlaSerGlyGlyLeuLeuLeuValAspGluAlaPheGlyAspLeu
    GAGCTTCTGGCGATCGCCGCAAGGCAGAAGGCGAGCGGCGGACTGCTGCTGGTCGATGAGGCCTTCGGCGATCTT
3731      3741      3751      3761      3771      3781      3791
    GluProGlnLeuSerValAlaGlyHisAlaSerGlyGlnGlyAsnLeuIleValPheArgSerPheGlyLysPhe
    GAGCCGCAACTGAGTGTCGCTGGTCACGCGTCAGGGCAAGGCAACCTCATCGTCTTCCGCTCCTTCGGCAAGTTC
3806      3816      3826      3836      3846      3856      3866
    PheGlyLeuAlaGlyLeuArgLeuGlyPheValValAlaThrGluProValLeuAlaSerPheAlaAspTrpLeu
    TTCGGCCTTGCGGGCCTGCGCCTCGGCTTCGTCGTTGCGACCGAGCCAGTGCTTGCATCCTTTGCCGATTGGCTC
3881      3891      3901      3911      3921      3931      3941
    GlyProTrpAlaValSerGlyProAlaLeuThrIleSerLysAlaLeuMetGlnGlyAspThrLysAlaIleAla
    GGTCCCTGGGCTGTCTCCGGCCCGGCGTTGACGATCTCGAAAGCGCTGATGCAGGGCGATACGAAGGCGATCGCG
3956      3966      3976      3986      3996      4006      4016
    AlaGlyIleLeuGluArgArgAlaGlyLeuAspAlaAlaLeuAspGlyAlaGlyLeuAsnArgIleGlyGlyThr
    GCGGGCATCCTCGAGCGTCGCGCCGGCCTCGATGCGGCTCTCGATGGGGCAGGGCTCAACCGTATCGGCGGCACG
4031      4041      4051      4061      4071      4081      4091
    GlyLeuPheValLeuValGluHisProArgAlaAlaLeuLeuGlnGluArgLeuCysGluAlaHisIleLeuThr
    GGGCTATTCGTGCTGGTCGAGCATCCCAGGGCAGCTCTGCTGCAGGAGCGGCTCTGCGAGGCCCATATTCTCACG
4106      4116      4126      4136      4146      4156      4166
    ArgLysPheAspTyrAlaProThrTrpLeuArgValGlyLeuAlaProAspAlaAlaGlyAspArgArgLeuAla
    CGCAAGTTCGACTATGCCCCGACCTGGCTCAGGGTCGGTCTTGCGCCTGACGCGGCTGGTGACCGACGGCTGGCG
4181      4191      4201      4211      4221      4231      4241
    AspAlaLeuAlaArgMetGluLeu***
    GACGCGCTTGCCCGCATGGAGCTCTGA
4256      4266      4276      4286      4296      4306      4316
```

FIG. 15F

NAME = COBC

FIRST RESIDUE = 1
LAST RESIDUE = 333

			NUMBER	NO. %	WEIGHT	WEIGHT %
1	PHE	F	11	3.30	1617.77	4.62
2	LEU	L	43	12.91	4862.44	13.90
3	ILE	I	13	3.90	1470.04	4.20
4	MET	M	3	0.90	393.12	1.12
5	VAL	V	24	7.21	2377.68	6.79
6	SER	S	11	3.30	957.33	2.74
7	PRO	P	23	6.91	2232.15	6.38
8	THR	T	14	4.20	1414.70	4.04
9	ALA	A	56	16.82	3978.24	11.37
10	TYR	Y	6	1.80	978.36	2.80
11	*	*	0	0.00	0.00	0.00
12	HIS	H	7	2.10	959.42	2.74
13	GLN	Q	8	2.40	1024.48	2.93
14	ASN	N	8	2.40	912.32	2.61
15	LYS	K	5	1.50	640.45	1.83
16	ASP	D	19	5.71	2185.57	6.25
17	GLU	E	15	4.50	1935.60	5.53
18	CYS	C	2	0.60	206.02	0.59
19	TRP	W	5	1.50	930.40	2.66
20	ARG	R	25	7.51	3902.50	11.15
21	GLY	G	35	10.51	1995.70	5.70
22	-	-	0	0.00	0.00	0.00

RESIDUES = 333
MOLECULAR WEIGHT = 34992.
INDEX OF POLARITY (%) = 34.
ISOELECTRIC POINT = 6.72
OD 260 (1mg/ml) = 0.670 OD 280 (1mg/ml) = 0.998

HYDROPHILICITY PROFILE OF THE COBC PROTEIN

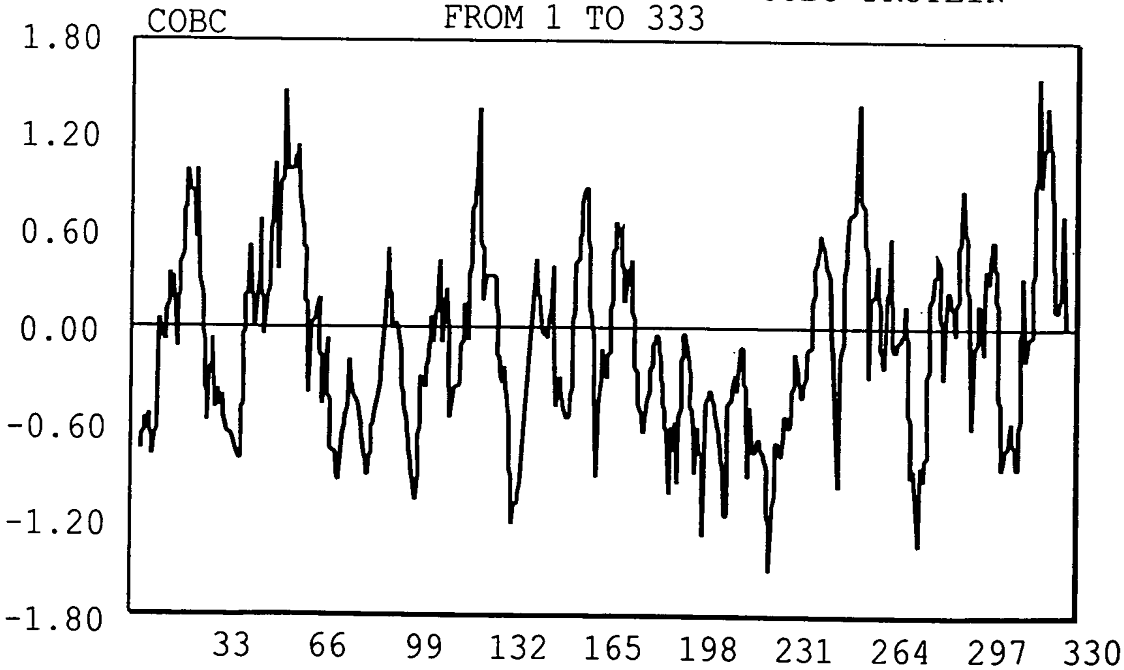


FIG. 15G

cobD GENE (SEQ ID NO: 9) AND COBD PROTEIN (SEQ ID NO: 10)
SEQUENCE OF THE 5396-BP ClaI-HindIII-HindIII-HindIII FRAGMENT
FROM 4284 TO 5252

```
    MetSerGluThrIleLeuLeuIleLeuAlaLeuAlaLeuValIleAspArgValValGlyAspProAspTrpLeu
    GTGTCGGAGACGATCCTGCTCATTCTCGCGCTGGCGCTGGTGATCGACCGCGTTGTCGGCGATCCGGACTGGCTC
4284      4294      4304      4314      4324      4334      4344
    TrpAlaArgValProHisProValValPhePheGlyLysAlaIleGlyPhePheAspAlaArgLeuAsnArgGlu
    TGGGCGCGCGTGCCGCATCCGGTCGTGTTTTTCGGCAAGGCCATCGGCTTTTTCGACGCGCGGCTGAACCGGGAG
4359      4369      4379      4389      4399      4409      4419
    AspLeuGluAspSerAlaArgLysPheArgGlyValValAlaIleLeuLeuLeuLeuGlyIleSerAlaTrpPhe
    GACCTCGAGGATAGCGCGCGCAAATTTCGTGGCGTCGTCGCGATCCTTTTGTTGCTTGGCATCAGCGCCTGGTTC
4434      4444      4454      4464      4474      4484      4494
    GlyHisLeuLeuHisArgLeuPheAlaValLeuGlyProLeuGlyPheLeuLeuGluAlaValLeuValAlaVal
    GGCCATCTGCTGCATCGCCTGTTCGCCGTCCTCGGACCGCTCGGCTTTCTGCTCGAGGCGGTTCTGGTCGCGGTC
4509      4519      4529      4539      4549      4559      4569
    PheLeuAlaGlnLysSerLeuAlaAspHisValArgArgValAlaGlyGlyLeuArgGlnGlyGlyLeuGluGly
    TTCCTGGCACAGAAGAGCCTCGCCGATCACGTGCGTCGCGTGGCCGGGGGCTTGCGACAGGGCGGGCTGGAAGGC
4584      4594      4604      4614      4624      4634      4644
    GlyArgAlaAlaValSerMetIleValGlyArgAspProLysThrLeuAspGluProAlaValCysArgAlaAla
    GGGCGTGCCGCCGTGTCGATGATCGTTGGTCGCGATCCAAAGACGCTCGACGAGCCGGCGGTCTGCCGTGCCGCG
4659      4669      4679      4689      4699      4709      4719
    IleGluSerLeuAlaGluAsnPheSerAspGlyValValAlaProAlaPheTrpTyrAlaValAlaGlyLeuPro
    ATCGAAAGCCTTGCCGAGAATTTCTCCGACGGCGTCGTGGCGCCGGCCTTCTGGTACGCGGTTGCCGGCCTGCCG
4734      4744      4754      4764      4774      4784      4794
    GlyLeuLeuAlaTyrLysMetLeuAsnThrAlaAspSerMetIleGlyHisLysSerProLysTyrLeuHisPhe
    GGGCTTCTTGCCTACAAGATGCTGAACACCGCCGATTCGATGATCGGCCACAAGTCGCCGAAATATCTGCACTTC
4809      4819      4829      4839      4849      4859      4869
    GlyTrpAlaSerAlaArgLeuAspAspLeuAlaAsnLeuProAlaAlaArgLeuSerIleLeuLeuIleSerAla
    GGCTGGGCCTCGGCCCGACTCGACGATCTCGCCAACCTGCCGGCAGCGAGGCTCTCGATCCTTTTGATCTCAGCC
4884      4894      4904      4914      4924      4934      4944
    GlyAlaLeuIleHisArgGlyAlaSerAlaAlaLysAspAlaLeuThrValAlaLeuArgAspHisGlyLeuHis
    GGTGCGCTGATCCATCGTGGCGCCAGCGCCGCCAAGGATGCGCTGACCGTGGCCCTTCGCGACCATGGCCTGCAC
4959      4969      4979      4989      4999      5009      5019
    ArgSerProAsnSerGlyTrpProGluAlaAlaMetAlaGlyAlaLeuAspLeuGlnLeuAlaGlyProArgIle
    CGCTCGCCGAACTCCGGCTGGCCGGAAGCGGCCATGGCCGGCGCGCTCGATCTGCAGCTTGCCGGTCCGCGGATC
5034      5044      5054      5064      5074      5084      5094
    TyrGlyGlyValLysValSerGluProMetIleAsnGlyProGlyArgAlaValAlaThrSerGluAspIleAsp
    TATGGCGGCGTCAAGGTCAGCGAACCTATGATCAACGGTCCGGGCCGAGCGGTTGCAACAAGCGAAGACATCGAC
5109      5119      5129      5139      5149      5159      5169
    AlaGlyIleAlaValPheTyrGlyAlaCysThrValMetAlaGlyPheValLeuAlaIleAlaMetIle***
    GCCGGTATTGCTGTATTTTATGGCGCCTGTACGGTCATGGCCGGGTTTGTTCTTGCAATCGCAATGATTTGA
5184      5194      5204      5214      5224      5234      5244
```

FIG. 15H

NAME = COBD

FIRST RESIDUE = 1
LAST RESIDUE = 323

			NUMBER	NO. %	WEIGHT	WEIGHT %
1	PHE	F	14	4.33	2058.98	6.02
2	LEU	L	45	13.93	5088.60	14.89
3	ILE	I	18	5.57	2035.44	5.96
4	MET	M	8	2.48	1048.32	3.07
5	VAL	V	27	8.36	2674.89	7.83
6	SER	S	17	5.26	1479.51	4.33
7	PRO	P	15	4.64	1455.75	4.26
8	THR	T	6	1.86	606.30	1.77
9	ALA	A	51	15.79	3623.04	10.60
10	TYR	Y	5	1.55	815.30	2.39
11	*	*	0	0.00	0.00	0.00
12	HIS	H	9	2.79	1233.54	3.61
13	GLN	Q	3	0.93	384.18	1.12
14	ASN	N	6	1.86	684.24	2.00
15	LYS	K	9	2.79	1152.81	3.37
16	ASP	D	18	5.57	2070.54	6.06
17	GLU	E	11	3.41	1419.44	4.15
18	CYS	C	2	0.62	206.02	0.60
19	TRP	W	6	1.86	1116.48	3.27
20	ARG	R	20	6.19	3122.00	9.14
21	GLY	G	33	10.22	1881.66	5.51
22	-	-	0	0.00	0.00	0.00

RESIDUES = 323
MOLECULAR WEIGHT = 34175.
INDEX OF POLARITY (%) = 31.
ISOELECTRIC POINT = 8.00
OD 260 (1mg/ml) = 0.789 OD 280 (1mg/ml) = 1.150

HYDROPHILICITY PROFILE OF THE COBD PROTEIN
COBD FROM 1 TO 323

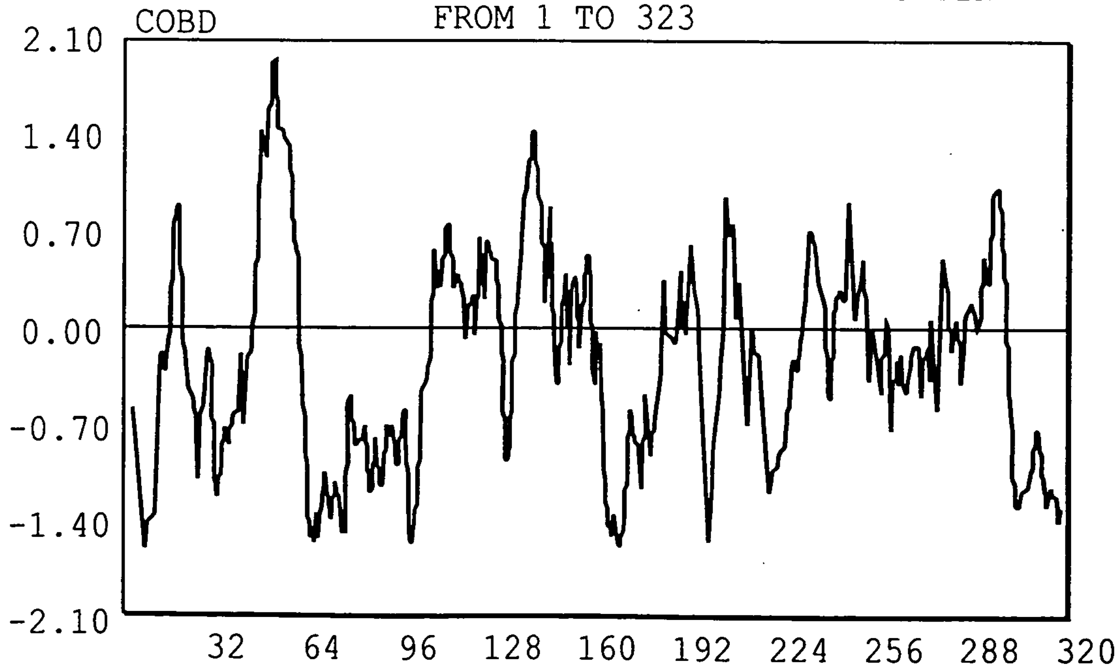


FIG. 15I

cobE GENE (SEQ ID NO: 11) AND COBE PROTEIN (SEQ ID NO: 12)
SEQUENCE OF THE 5396-BP ClaI-HindIII-HindIII-HindIII FRAGMENT
FROM 549 TO 1010

```
   MetProSerGlyGlnHisSerAlaGlnThrThrLysAlaGlyAlaGlyLeuValLeuGlyLeuGlyCysGluArg
   ATGCCATCGGGCCAACACTCTGCACAGACGACGAAAGCAGGAGCCGGGCTGGTGCTCGGGCTCGGCTGCGAGCGT
549       559       569       579       589       599       609
   ArgThrProAlaGluGluValIleAlaLeuAlaGluArgAlaLeuAlaAspAlaGlyValAlaProGlyAspLeu
   CGCACGCCGGCCGAAGAGGTGATCGCCCTTGCCGAGCGTGCGCTTGCCGATGCCGGTGTTGCGCCCGGCGATCTG
624       634       644       654       664       674       684
   ArgLeuValAlaSerLeuAspAlaArgAlaGluGluProAlaIleLeuAlaAlaAlaGlnHisPheAlaValPro
   CGGCTGGTCGCCTCGCTCGATGCTCGCGCCGAGGAGCCGGCGATCCTGGCGGCCGCTCAGCATTTCGCGGTTCCG
699       709       719       729       739       749       759
   AlaAlaPheTyrAspAlaAlaThrLeuGluAlaGluAlaSerArgLeuAlaAsnProSerGluIleValPheAla
   GCCGCGTTCTACGATGCCGCCACGCTCGAAGCCGAAGCTTCCCGGCTCGCCAACCCGTCCGAGATCGTCTTTGCC
774       784       794       804       814       824       834
   TyrThrGlyCysHisGlyValAlaGluGlyAlaAlaLeuValGlyAlaGlyArgGluAlaValLeuIleValGln
   TACACGGGTTGTCATGGCGTTGCCGAGGGTGCAGCGCTCGTCGGCGCCGGTCGCGAAGCCGTGCTGATTGTGCAG
849       859       869       879       889       899       909
   LysIleValSerAlaHisAlaThrAlaAlaLeuAlaGlyProAlaThrLeuArgAlaGluLysArgIleGlnAla
   AAGATCGTCTCCGCCCATGCGACGGCCGCACTTGCCGGGCCGGCGACCTTGCGCGCCGAAAAGCGCATCCAGGCG
924       934       944       954       964       974       984
   AlaGluAlaVal***
   GCGGAGGCTGTCTGA
999       1009      1019      1029      1039      1049      1059
```

FIG. 15J

NAME = COBE

FIRST RESIDUE = 1
LAST RESIDUE = 154

			NUMBER	NO. %	WEIGHT	WEIGHT %
1	PHE	F	3	1.95	441.21	2.85
2	LEU	L	15	9.74	1696.20	10.96
3	ILE	I	6	3.90	678.48	4.38
4	MET	M	1	0.65	131.04	0.85
5	VAL	V	12	7.79	1188.84	7.68
6	SER	S	6	3.90	522.18	3.37
7	PRO	P	7	4.55	679.35	4.39
8	THR	T	7	4.55	707.35	4.57
9	ALA	A	41	26.62	2912.64	18.82
10	TYR	Y	2	1.30	326.12	2.11
11	*	*	0	0.00	0.00	0.00
12	HIS	H	4	2.60	548.24	3.54
13	GLN	Q	5	3.25	640.30	4.14
14	ASN	N	1	0.65	114.04	0.74
15	LYS	K	3	1.95	384.27	2.48
16	ASP	D	4	2.60	460.12	2.97
17	GLU	E	13	8.44	1677.52	10.84
18	CYS	C	2	1.30	206.02	1.33
19	TRP	W	0	0.00	0.00	0.00
20	ARG	R	9	5.84	1404.90	9.08
21	GLY	G	13	8.44	741.26	4.79
22	-	-	0	0.00	0.00	0.00

RESIDUES = 154
MOLECULAR WEIGHT = 15478.
INDEX OF POLARITY (%) = 34.
ISOELECTRIC POINT = 5.61
OD 260 (1mg/ml) = 0.113 OD 280 (1mg/ml) = 0.154

HYDROPHILICITY PROFILE OF THE COBE PROTEIN
FROM 1 TO 154

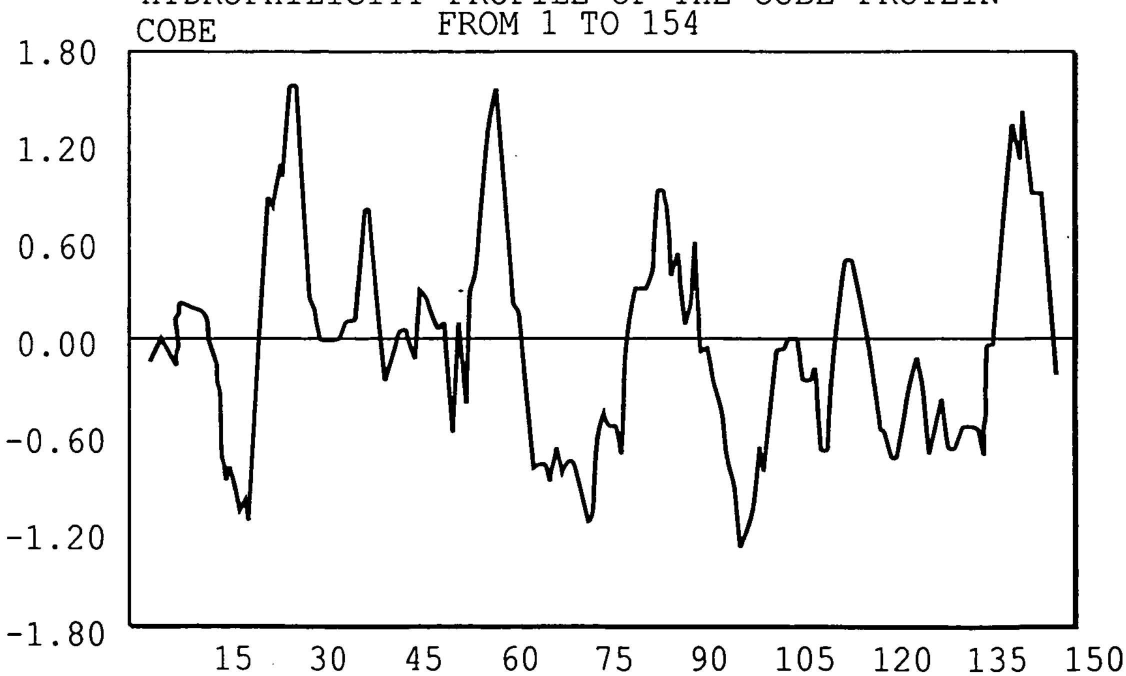


FIG. 15K

cobF GENE (SEQ ID NO: 13) AND COBF PROTEIN (SEQ ID NO: 14)
SEQUENCE OF THE 8753-BP FRAGMENT FROM 736 TO 1521

```
 MetAlaGluAlaGlyMetArgLysIleLeuIleIleGlyIleGlySerGlyAsnProGluHisMetThrValGln
 ATGGCGGAGGCGGGCATGCGCAAAATTCTGATCATCGGCATCGGTTCGGGCAATCCCGAACACATGACCGTGCAG
736       746       756       766       776       786       796
 AlaIleAsnAlaLeuAsnCysAlaAspValLeuPheIleProThrLysGlyAlaLysLysThrGluLeuAlaGlu
 GCGATCAACGCGCTGAACTGCGCCGACGTGCTCTTTATCCCGACCAAGGGAGCGAAGAAGACCGAGCTTGCCGAA
811       821       831       841       851       861       871
 ValArgArgAspIleCysAlaArgTyrValThrArgLysAspSerArgThrValGluPheAlaValProValArg
 GTGCGCCGCGACATCTGCGCCCGCTACGTCACGCGCAAGGACAGCCGCACCGTCGAGTTCGCGGTGCCCGTGCGG
886       896       906       916       926       936       946
 ArgThrGluGlyValSerTyrAspGlySerValAspAspTrpHisAlaGlnIleAlaGlyIleTyrGluAlaLeu
 CGCACCGAAGGCGTCAGCTATGACGGCAGCGTCGATGACTGGCACGCCCAGATCGCTGGGATTTACGAAGCGCTT
961       971       981       991       1001      1011      1021
 LeuSerLysGluLeuGlyGluGluGlyThrGlyAlaPheLeuValTrpGlyAspProMetLeuTyrAspSerThr
 CTATCGAAGGAGTTGGGCGAAGAGGGAACTGGCGCGTTTCTCGTCTGGGGCGACCCGATGCTCTATGACAGCACC
1036      1046      1056      1066      1076      1086      1096
 IleArgIleValGluArgValLysAlaArgGlyGluValAlaPheAlaTyrAspValIleProGlyIleThrSer
 ATTCGCATCGTCGAGCGGGTCAAGGCACGCGGTGAGGTCGCCTTCGCCTACGACGTCATTCCCGGGATCACCAGT
1111      1121      1131      1141      1151      1161      1171
 LeuGlnAlaLeuCysAlaSerHisArgIleProLeuAsnLeuValGlyLysProValGluIleThrThrGlyArg
 CTGCAGGCGCTTTGCGCCAGCCACCGCATTCCGCTGAACCTCGTCGGCAAGCCGGTGGAGATCACCACGGGGCGT
1186      1196      1206      1216      1226      1236      1246
 ArgLeuHisGluSerPheProGluLysSerGlnThrSerValValMetLeuAspGlyGluGlnAlaPheGlnArg
 CGGCTGCACGAAAGCTTTCCCGAGAAGAGCCAGACCTCGGTCGTCATGCTCGATGGCGAACAGGCGTTTCAGCGG
1261      1271      1281      1291      1301      1311      1321
 ValGluAspProGluAlaGluIleTyrTrpGlyAlaTyrLeuGlyThrArgAspGluIleValIleSerGlyArg
 GTCGAGGACCCGGAGGCGGAGATCTATTGGGGCGCCTATCTCGGCACGCGGGATGAGATCGTCATTTCCGGCCGC
1336      1346      1356      1366      1376      1386      1396
 ValAlaGluValLysAspArgIleLeuGluThrArgAlaAlaAlaArgAlaLysMetGlyTrpIleMetAspIle
 GTGGCTGAGGTGAAGGACCGGATCCTTGAAACGCGGGCGGCGGCGCGCGCGAAGATGGGATGGATCATGGACATC
1411      1421      1431      1441      1451      1461      1471
 TyrLeuLeuArgLysGlyAlaAspPheAspGlu***
 TATCTCCTGCGCAAGGGCGCCGACTTCGACGAGTGA
1486      1496      1506      1516
```

FIG. 16A

COBF PROTEIN

FIRST RESIDUE = 1
LAST RESIDUE = 261

			NUMBER	NO. %	WEIGHT	WEIGHT %
1	PHE	F	7	2.68	1029.49	3.56
2	LEU	L	19	7.28	2148.52	7.43
3	ILE	I	21	8.05	2374.68	8.21
4	MET	M	7	2.68	917.28	3.17
5	VAL	V	22	8.43	2179.54	7.53
6	SER	S	12	4.60	1044.36	3.61
7	PRO	P	9	3.45	873.45	3.02
8	THR	T	14	5.36	1414.70	4.89
9	ALA	A	27	10.34	1918.08	6.63
10	TYR	Y	8	3.07	1304.48	4.51
11	*	*	0	0.00	0.00	0.00
12	HIS	H	4	1.53	548.24	1.90
13	GLN	Q	6	2.30	768.36	2.66
14	ASN	N	4	1.53	456.16	1.58
15	LYS	K	12	4.60	1537.08	5.31
16	ASP	D	16	6.13	1840.48	6.36
17	GLU	E	23	8.81	2967.92	10.26
18	CYS	C	3	1.15	309.03	1.07
19	TRP	W	4	1.53	744.32	2.57
20	ARG	R	21	8.05	3278.10	11.33
21	GLY	G	22	8.43	1254.44	4.34

RESIDUES = 261
MOLECULAR WEIGHT = 28927.
INDEX OF POLARITY (%) = 43.
ISOELECTRIC POINT = 5.70
OD 260 (1mg/ml) = 0.705 OD 280 (1mg/ml) = 1.097

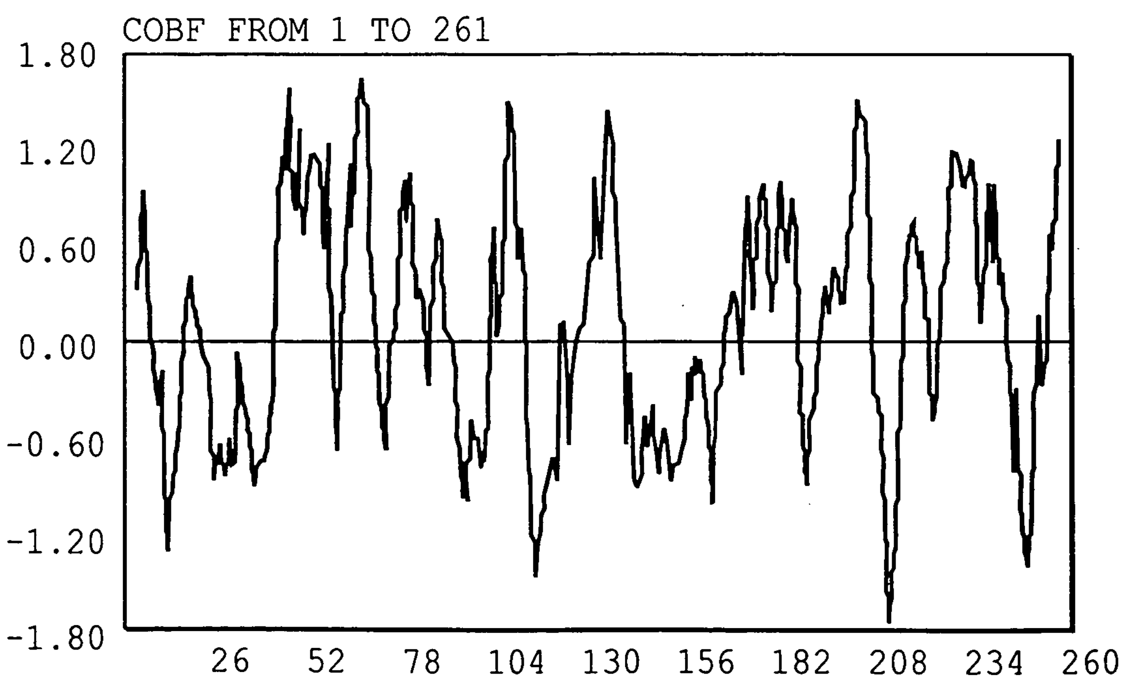


FIG. 16B

cobG GENE (SEQ ID NO: 15) AND COBG PROTEIN (SEQ ID NO: 16)
SEQUENCE OF THE 8753-BP FRAGMENT FROM 1620 TO 2999

```
   MetThrAspLeuMetThrSerCysAlaLeuProLeuThrGlyAspAlaGlyThrValAlaSerMetArgArgGly
   ATGACGGATTTGATGACCAGCTGCGCCCTTCCATTGACCGGAGATGCCGGCACCGTCGCTTCGATGCGCCGCGGC
1620      1630      1640      1650      1660      1670      1680
   AlaCysProSerLeuAlaGluProMetGlnThrGlyAspGlyLeuLeuValArgValArgProThrAspAspSer
   GCCTGCCCGTCCTTGGCAGAGCCGATGCAGACCGGCGACGGCCTGCTCGTGAGGGTGAGGCCAACGGATGACAGC
1695      1705      1715      1725      1735      1745      1755
   LeuThrLeuProLysValIleAlaLeuAlaThrAlaAlaGluArgPheGlyAsnGlyIleIleGluIleThrAla
   CTGACGCTGCCGAAGGTCATTGCCCTTGCCACGGCTGCCGAGCGCTTCGGCAATGGCATCATCGAGATTACCGCG
1770      1780      1790      1800      1810      1820      1830
   ArgGlyAsnLeuGlnLeuArgGlyLeuSerAlaAlaSerValProArgLeuAlaGlnAlaIleGlyAspAlaGlu
   CGCGGAAACCTGCAGCTTCGCGGCCTGAGCGCGGCTTCGGTGCCAAGGCTGGCGCAGGCGATCGGCGATGCGGAG
1845      1855      1865      1875      1885      1895      1905
   IleAlaIleAlaGluGlyLeuAlaIleGluValProProLeuAlaGlyIleAspProAspGluIleAlaAspPro
   ATCGCCATTGCCGAGGGGCTCGCGATCGAGGTGCCGCCCCTGGCCGGCATCGACCCGGACGAGATCGCCGATCCG
1920      1930      1940      1950      1960      1970      1980
   ArgProIleAlaThrGluLeuArgGluAlaLeuAspValArgGlnValProLeuLysLeuAlaProLysLeuSer
   CGGCCGATTGCCACTGAGCTTCGTGAAGCGTTGGATGTGCGCCAGGTGCCGTTGAAGCTTGCACCCAAATTATCC
1995      2005      2015      2025      2035      2045      2055
   ValValIleAspSerGlyGlyArgPheGlyLeuGlyAlaValValAlaAspIleArgLeuGlnAlaValSerThr
   GTCGTCATCGATAGCGGTGGCCGGTTTGGTCTCGGCGCTGTCGTCGCCGACATTCGCCTTCAGGCGGTTTCGACT
2070      2080      2090      2100      2110      2120      2130
   ValAlaGlyValAlaTrpValLeuSerLeuGlyGlyThrSerThrLysAlaSerSerValGlyThrLeuAlaGly
   GTCGCGGGGGTGGCCTGGGTGCTGTCGCTTGGCGGCACGTCAACGAAGGCATCGAGCGTCGGGACGTTGGCCGGC
2145      2155      2165      2175      2185      2195      2205
   AsnAlaValValProAlaLeuIleThrIleLeuGluLysLeuAlaSerLeuGlyThrThrMetArgGlyArgAsp
   AACGCGGTCGTGCCGGCCCTGATCACCATTCTCGAGAAACTGGCGAGCCTGGGCACGACGATGCGCGGGCGCGAT
2220      2230      2240      2250      2260      2270      2280
   LeuAspProSerGluIleArgAlaLeuCysArgCysGluThrSerSerGluArgProAlaAlaProArgSerAla
   CTGGACCCGTCGGAAATCCGCGCGCTCTGTCGCTGTGAGACATCGTCCGAACGCCCGGCCGCTCCGCGTTCGGCC
2295      2305      2315      2325      2335      2345      2355
   AlaIleProGlyIleHisAlaLeuGlyAsnAlaAspThrValLeuGlyLeuGlyLeuAlaPheAlaGlnValGlu
   GCAATACCCGGCATTCATGCGCTGGGTAACGCCGACACCGTTCTCGGCCTCGGTCTGGCCTTTGCTCAGGTGGAG
2370      2380      2390      2400      2410      2420      2430
   AlaAlaAlaLeuAlaSerTyrLeuHisGlnValGlnAlaLeuGlyAlaAsnAlaIleArgLeuAlaProGlyHis
   GCCGCCGCGCTGGCATCCTACCTGCATCAGGTCCAGGCGCTTGGCGCCAATGCGATCCGGCTTGCGCCCGGGCAC
2445      2455      2465      2475      2485      2495      2505
```

FIG. 16C

```
     AlaPhePheValLeuGlyLeuCysProGluThrAlaAlaValAlaGlnSerLeuAlaAlaSerHisGlyPheArg
     GCCTTCTTCGTCCTCGGCCTTTGCCCCGAGACCGCGGCTGTGGCGCAGAGCCTGGCAGCGTCACACGGTTTTCGC
2520      2530      2540      2550      2560      2570      2580
     IleAlaGluGlnAspProArgAsnAlaIleAlaThrCysAlaGlySerLysGlyCysAlaSerAlaTrpMetGlu
     ATTGCCGAGCAGGATCCGCGCAATGCGATCGCCACCTGCGCCGGCAGCAAGGGTTGCGCCTCGGCGTGGATGGAA
2595      2605      2615      2625      2635      2645      2655
     ThrLysGlyMetAlaGluArgLeuValGluThrAlaProGluLeuLeuAspGlySerLeuThrValHisLeuSer
     ACCAAGGGCATGGCCGAGCGCCTCGTCGAGACGGCGCCGGAATTGCTCGACGGGTCGCTCACCGTGCATCTCTCC
2670      2680      2690      2700      2710      2720      2730
     GlyCysAlaLysGlyCysAlaArgProLysProSerGluLeuThrLeuValGlyAlaProSerGlyTyrGlyLeu
     GGCTGCGCCAAGGGCTGCGCCCGGCCGAAGCCGTCCGAACTGACGCTTGTCGGTGCGCCATCAGGATACGGGCTT
2745      2755      2765      2775      2785      2795      2805
     ValValAsnGlyAlaAlaAsnGlyLeuProSerAlaTyrThrAspGluAsnGlyMetGlySerAlaLeuAlaArg
     GTCGTAAATGGGGCTGCCAATGGCTTGCCAAGCGCCTACACCGATGAGAATGGAATGGGATCCGCCCTTGCCCGG
2820      2830      2840      2850      2860      2870      2880
     LeuGlyArgLeuValArgGlnAsnLysAspAlaGlyGluSerAlaGlnSerCysLeuThrArgLeuGlyAlaAla
     CTCGGCCGGCTGGTGCGGCAAAACAAAGACGCTGGCGAATCGGCGCAGTCCTGTCTTACACGGCTCGGAGCTGCG
2895      2905      2915      2925      2935      2945      2955
     ArgValSerAlaAlaPheGluGlnGly***
     CGCGTCTCGGCAGCGTTCGAACAGGGATAG
2970      2980      2990      3000
```

FIG. 16D

COBG PROTEIN

FIRST RESIDUE = 1
LAST RESIDUE = 459

			NUMBER	NO. %	WEIGHT	WEIGHT %
1	PHE	F	7	1.53	1029.49	2.21
2	LEU	L	56	12.20	6332.48	13.57
3	ILE	I	21	4.58	2374.68	5.09
4	MET	M	8	1.74	1048.32	2.25
5	VAL	V	31	6.75	3071.17	6.58
6	SER	S	32	6.97	2784.96	5.97
7	PRO	P	26	5.66	2523.30	5.41
8	THR	T	27	5.88	2728.35	5.85
9	ALA	A	78	16.99	5541.12	11.88
10	TYR	Y	3	0.65	489.18	1.05
11	*	*	0	0.00	0.00	0.00
12	HIS	H	5	1.09	685.30	1.47
13	GLN	Q	13	2.83	1664.78	3.57
14	ASN	N	10	2.18	1140.40	2.44
15	LYS	K	10	2.18	1280.90	2.75
16	ASP	D	19	4.14	2185.57	4.68
17	GLU	E	24	5.23	3096.96	6.64
18	CYS	C	10	2.18	1030.10	2.21
19	TRP	W	2	0.44	372.16	0.80
20	ARG	R	29	6.32	4526.90	9.70
21	GLY	G	48	10.46	2736.96	5.87
22	-	-	0	0.00	0.00	0.00

RESIDUES = 459
MOLECULAR WEIGHT = 46661.
INDEX OF POLARITY (%) = 37.
ISOELECTRIC POINT = 6.41
OD 260 (1mg/ml) = 0.215 OD 280 (1mg/ml) = 0.315

COBG FROM 1 TO 459

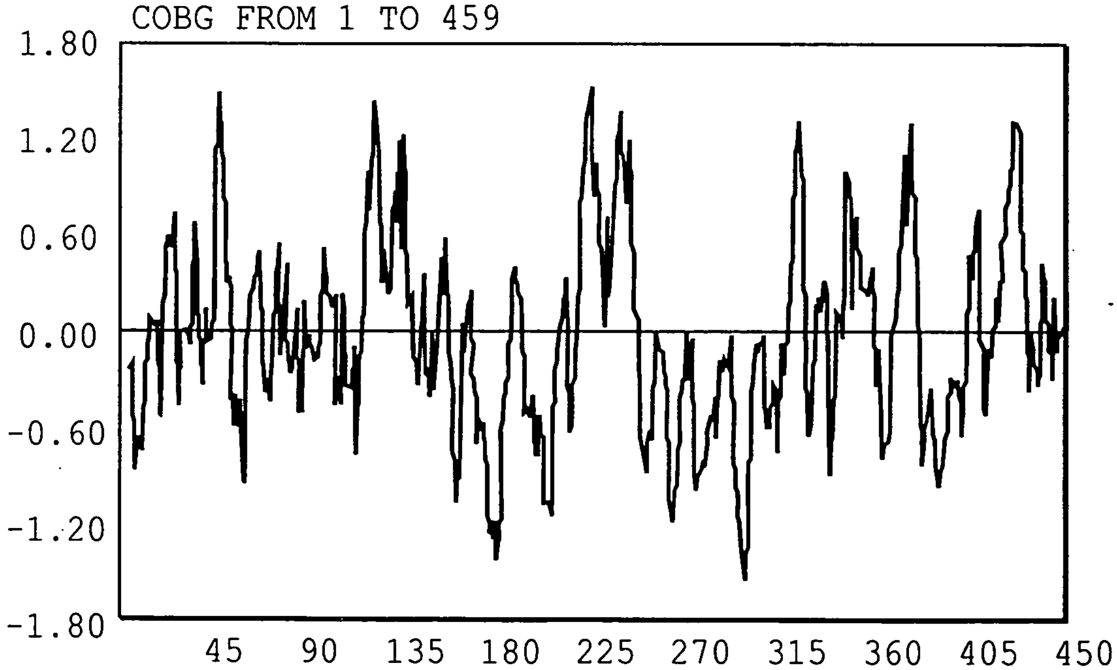


FIG. 16E

cobH GENE (SEQ ID NO: 17) AND COBH PROTEIN (SEQ ID NO: 18)
SEQUENCE OF THE 8753-BP FRAGMENT FROM 3002 TO 3634

```
    MetProGluTyrAspTyrIleArgAspGlyAsnAlaIleTyrGluArgSerPheAlaIleIleArgAlaGluAla
    ATGCCTGAGTATGATTACATTCGCGATGGCAACGCCATCTACGAGCGTTCCTTCGCCATCATCCGCGCCGAGGCC
3002      3012      3022      3032      3042      3052      3062
    AspLeuSerArgPheSerGluGluGluAlaAspLeuAlaValArgMetValHisAlaCysGlySerValGluAla
    GATCTGTCGCGCTTCTCCGAAGAGGAAGCGGATCTGGCTGTGCGCATGGTGCACGCCTGCGGTTCCGTCGAGGCG
3077      3087      3097      3107      3117      3127      3137
    ThrArgGlnPheValPheSerProAspPheValSerSerAlaArgAlaAlaLeuLysAlaGlyAlaProIleLeu
    ACCAGGCAGTTCGTGTTTTCTCCCGATTTCGTAAGCTCGGCCCGTGCGGCGCTGAAAGCCGGTGCGCCGATCCTC
3152      3162      3172      3182      3192      3202      3212
    CysAspAlaGluMetValAlaHisGlyValThrArgAlaArgLeuProAlaGlyAsnGluValIleCysThrLeu
    TGCGATGCCGAGATGGTTGCGCACGGTGTCACCCGCGCCCGTCTGCCGGCCGGCAACGAGGTGATCTGCACGCTG
3227      3237      3247      3257      3267      3277      3287
    ArgAspProArgThrProAlaLeuAlaAlaGluIleGlyAsnThrArgSerAlaAlaAlaLeuLysLeuTrpSer
    CGCGATCCTCGCACGCCCGCACTTGCGGCCGAGATCGGCAACACCCGCTCCGCCGCAGCCCTGAAGCTCTGGAGC
3302      3312      3322      3332      3342      3352      3362
    GluArgLeuAlaGlySerValValAlaIleGlyAsnAlaProThrAlaLeuPhePheLeuLeuGluMetLeuArg
    GAGCGGCTGGCCGGTTCGGTGGTCGCGATCGGCAACGCGCCGACGGCGTTGTTCTTCCTCTTGGAAATGCTGCGC
3377      3387      3397      3407      3417      3427      3437
    AspGlyAlaProLysProAlaAlaIleLeuGlyMetProValGlyPheValGlyAlaAlaGluSerLysAspAla
    GACGGCGCGCCGAAGCCGGCGGCAATCCTCGGCATGCCCGTCGGTTTCGTCGGTGCGGCGGAATCGAAGGATGCG
3452      3462      3472      3482      3492      3502      3512
    LeuAlaGluAsnSerTyrGlyValProPheAlaIleValArgGlyArgLeuGlyGlySerAlaMetThrAlaAla
    CTGGCCGAGAACTCCTATGGCGTTCCCTTCGCCATCGTGCGCGGCCGCCTCGGCGGGAGTGCCATGACGGCGGCA
3527      3537      3547      3557      3567      3577      3587
    AlaLeuAsnSerLeuAlaArgProGlyLeu***
    GCGCTTAACTCGCTCGCGAGGCCGGGCCTGTGA
3602      3612      3622      3632
```

FIG. 16F

COBH PROTEIN

FIRST RESIDUE = 1
LAST RESIDUE = 210

			NUMBER	NO. %	WEIGHT	WEIGHT %
1	PHE	F	9	4.29	1323.63	6.00
2	LEU	L	20	9.52	2261.60	10.26
3	ILE	I	10	4.76	1130.80	5.13
4	MET	M	6	2.86	786.24	3.57
5	VAL	V	14	6.67	1386.98	6.29
6	SER	S	14	6.67	1218.42	5.53
7	PRO	P	12	5.71	1164.60	5.28
8	THR	T	7	3.33	707.35	3.21
9	ALA	A	40	19.05	2841.60	12.89
10	TYR	Y	4	1.90	652.24	2.96
11	*	*	0	0.00	0.00	0.00
12	HIS	H	2	0.95	274.12	1.24
13	GLN	Q	1	0.48	128.06	0.58
14	ASN	N	6	2.86	684.24	3.10
15	LYS	K	4	1.90	512.36	2.32
16	ASP	D	9	4.29	1035.27	4.70
17	GLU	E	14	6.67	1806.56	8.19
18	CYS	C	3	1.43	309.03	1.40
19	TRP	W	1	0.48	186.08	0.84
20	ARG	R	17	8.10	2653.70	12.03
21	GLY	G	17	8.10	969.34	4.40
22	-	-	0	0.00	0.00	0.00

RESIDUES = 210
MOLECULAR WEIGHT = 22050.
INDEX OF POLARITY (%) = 35.
ISOELECTRIC POINT = 6.22
OD 260 (1mg/ml) = 0.291 OD 280 (1mg/ml) = 0.467

COBH FROM 1 TO 210

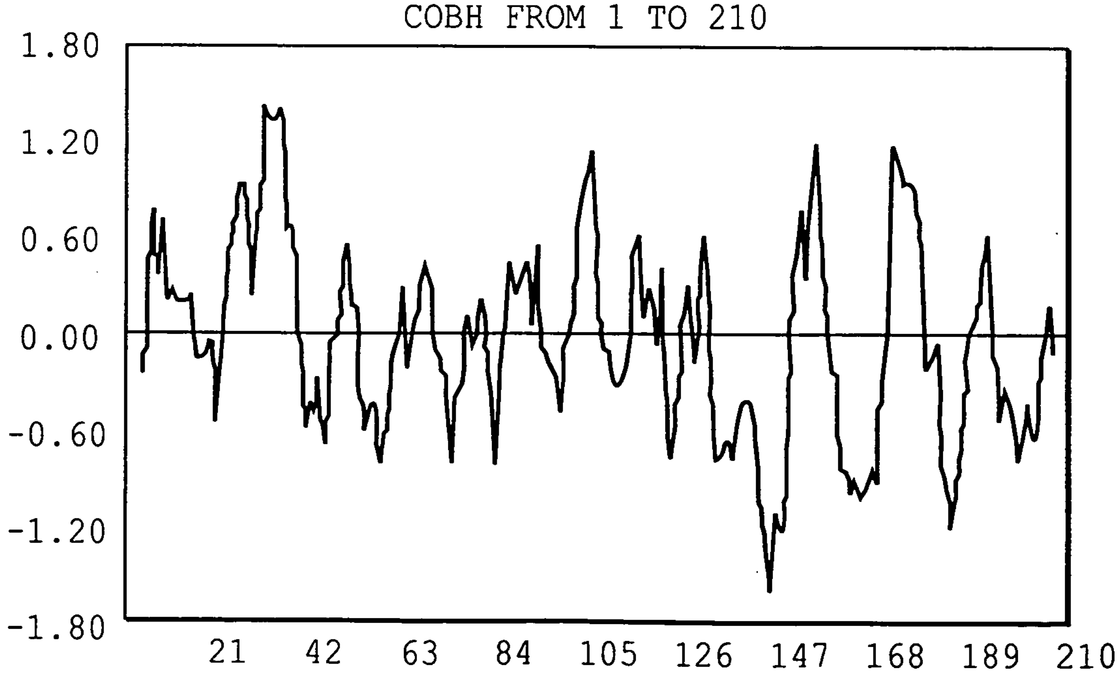


FIG. 16G

<u>cobI</u> GENE (SEQ ID NO: 19) AND COBI PROTEIN (SEQ ID NO: 20)
SEQUENCE OF THE 8753-BP FRAGMENT FROM 3631 TO 4368

```
   MetSerGlyValGlyValGlyArgLeuIleGlyValGlyThrGlyProGlyAspProGluLeuLeuThrValLys
   GTGAGCGGCGTCGGCGTGGGGCGCCTGATCGGTGTTGGGACCGGCCCCGGTGATCCGGAACTTTTGACGGTCAAG
3631      3641      3651      3661      3671      3681      3691
   AlaValLysAlaLeuGlyGlnAlaAspValLeuAlaTyrPheAlaLysAlaGlyArgSerGlyAsnGlyArgAla
   GCGGTGAAGGCGCTCGGGCAAGCCGATGTGCTTGCCTATTTCGCCAAGGCCGGGCGAAGCGGTAACGGCCGCGCG
3706      3716      3726      3736      3746      3756      3766
   ValValGluGlyLeuLeuLysProAspLeuValGluLeuProLeuTyrTyrProValThrThrGluIleAspLys
   GTGGTCGAGGGTCTGCTGAAGCCCGATCTTGTCGAGCTGCCGCTATACTATCCGGTGACGACCGAAATCGACAAG
3781      3791      3801      3811      3821      3831      3841
   AspAspGlyAlaTyrLysThrGlnIleThrAspPheTyrAsnAlaSerAlaGluAlaValAlaAlaHisLeuAla
   GACGATGGCGCCTACAAGACCCAGATCACCGACTTCTACAATGCGTCGGCCGAAGCGGTAGCGGCGCATCTTGCC
3856      3866      3876      3886      3896      3906      3916
   AlaGlyArgThrValAlaValLeuSerGluGlyAspProLeuPheTyrGlySerTyrMetHisLeuHisValArg
   GCCGGGCGCACGGTCGCCGTGCTCAGTGAAGGCGACCCGCTGTTCTATGGTTCCTACATGCATCTGCATGTGCGG
3931      3941      3951      3961      3971      3981      3991
   LeuAlaAsnArgPheProValGluValIleProGlyIleThrAlaMetSerGlyCysTrpSerLeuAlaGlyLeu
   CTCGCCAATCGTTTCCCGGTCGAGGTGATCCCCGGCATTACCGCCATGTCCGGCTGTTGGTCGCTTGCCGGCCTG
4006      4016      4026      4036      4046      4056      4066
   ProLeuValGlnGlyAspAspValLeuSerValLeuProGlyThrMetAlaGluAlaGluLeuGlyArgArgLeu
   CCGCTGGTGCAGGGCGACGACGTGCTCTCGGTGCTTCCGGGCACCATGGCCGAGGCCGAGCTCGGCCGCAGGCTT
4081      4091      4101      4111      4121      4131      4141
   AlaAspThrGluAlaAlaValIleMetLysValGlyArgAsnLeuProLysIleArgArgAlaLeuAlaAlaSer
   GCGGATACCGAAGCCGCCGTGATCATGAAGGTCGGGCGCAATTTGCCGAAGATCCGTCGGGCGCTCGCTGCCTCC
4156      4166      4176      4186      4196      4206      4216
   GlyArgLeuAspGlnAlaValTyrValGluArgGlyThrMetLysAsnAlaAlaMetThrAlaLeuAlaGluLys
   GGCCGTCTCGACCAGGCCGTCTATGTCGAACGCGGCACGATGAAGAACGCGGCGATGACGGCTCTTGCGGAAAAG
4231      4241      4251      4261      4271      4281      4291
   AlaAspAspGluAlaProTyrPheSerLeuValLeuValProGlyTrpLysAspArgPro***
   GCCGACGACGAGGCGCCCTATTTCTCGCTGGTGCTCGTTCCCGGCTGGAAGGACCGACCATGA
4306      4316      4326      4336      4346      4356      4366
```

FIG. 16H

COBI PROTEIN

FIRST RESIDUE = 1
LAST RESIDUE = 245

			NUMBER	NO. %	WEIGHT	WEIGHT %
1	PHE	F	5	2.04	735.35	2.84
2	LEU	L	28	11.43	3166.24	12.24
3	ILE	I	7	2.86	791.56	3.06
4	MET	M	7	2.86	917.28	3.54
5	VAL	V	25	10.20	2476.75	9.57
6	SER	S	10	4.08	870.30	3.36
7	PRO	P	14	5.71	1358.70	5.25
8	THR	T	12	4.90	1212.60	4.69
9	ALA	A	34	13.88	2415.36	9.33
10	TYR	Y	9	3.67	1467.54	5.67
11	*	*	0	0.00	0.00	0.00
12	HIS	H	3	1.22	411.18	1.59
13	GLN	Q	4	1.63	512.24	1.98
14	ASN	N	5	2.04	570.20	2.20
15	LYS	K	11	4.49	1408.99	5.44
16	ASP	D	15	6.12	1725.45	6.67
17	GLU	E	13	5.31	1677.52	6.48
18	CYS	C	1	0.41	103.01	0.40
19	TRP	W	2	0.82	372.16	1.44
20	ARG	R	14	5.71	2185.40	8.44
21	GLY	G	26	10.61	1482.52	5.73
22	-	-	0	0.00	0.00	0.00

RESIDUES = 245
MOLECULAR WEIGHT = 25878.
INDEX OF POLARITY (%) = 36.
ISOELECTRIC POINT = 6.17
OD 260 (1 mg/ml) = 0.512 OD 280 (1 mg/ml) = 0.843

COBI FROM 1 TO 245

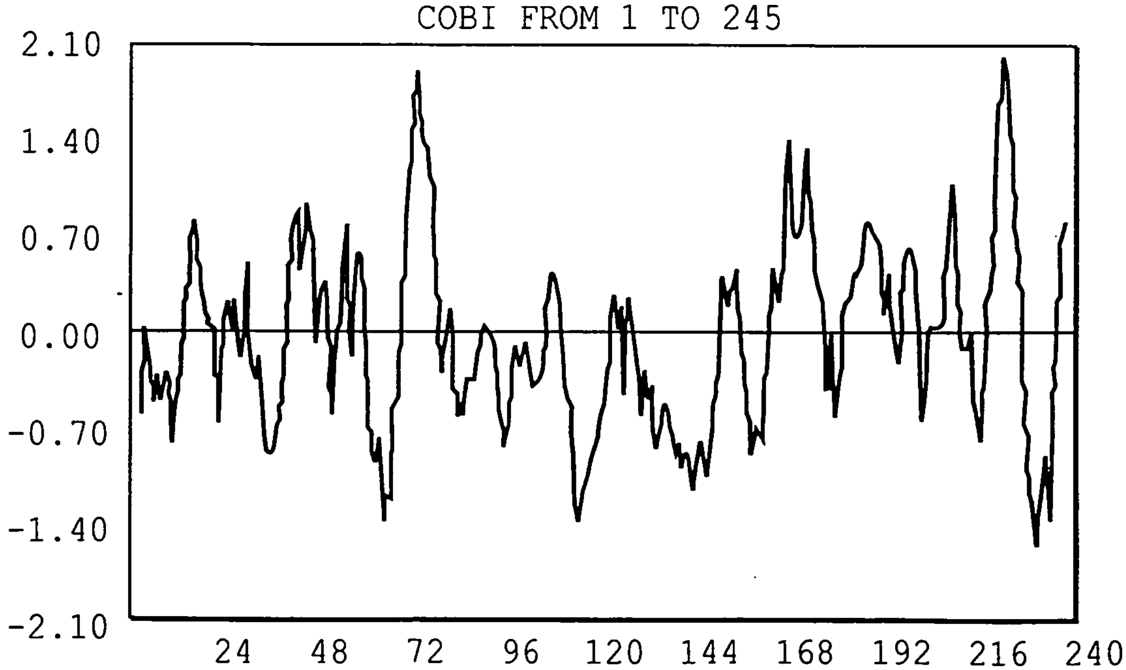


FIG. 16I

cobJ GENE (SEQ ID NO: 21) AND COBJ PROTEIN (SEQ ID NO: 22)
SEQUENCE OF THE 8753-BP FRAGMENT FROM 4365 TO 5129.

```
  MetThrGlyThrLeuTyrValValGlyThrGlyProGlySerAlaLysGlnMetThrProGluThrAlaGluAla
  ATGACCGGTACGCTCTATGTCGTCGGTACCGGACCGGGCAGCGCCAAGCAGATGACGCCGGAAACGGCGGAAGCC
4365      4375      4385      4395      4405      4415      4425
  ValAlaAlaAlaGlnGluPheTyrGlyTyrPheProTyrLeuAspArgLeuAsnLeuArgProAspGlnIleArg
  GTTGCGGCCGCTCAGGAGTTTTACGGCTACTTTCCCTATCTCGACCGGCTGAACCTCAGACCGGATCAGATCCGT
4440      4450      4460      4470      4480      4490      4500
  ValAlaSerAspAsnArgGluGluLeuAspArgAlaGlnValAlaLeuThrArgAlaAlaAlaGlyValLysVal
  GTCGCCTCGGACAACCGCGAGGAGCTCGATCGGGCACAGGTCGCGCTGACGCGGGCTGCGGCAGGCGTGAAGGTC
4515      4525      4535      4545      4555      4565      4575
  CysMetValSerGlyGlyAspProGlyValPheAlaMetAlaAlaAlaValCysGluAlaIleAspLysGlyPro
  TGCATGGTCTCCGGTGGCGATCCCGGTGTCTTTGCCATGGCGGCCGCCGTCTGCGAGGCGATCGACAAGGGACCG
4590      4600      4610      4620      4630      4640      4650
  AlaGluTrpLysSerValGluLeuValIleThrProGlyValThrAlaMetLeuAlaValAlaAlaArgIleGly
  GCGGAATGGAAGTCGGTTGAACTGGTGATCACGCCCGGCGTGACCGCGATGCTCGCCGTTGCCGCCCGCATCGGC
4665      4675      4685      4695      4705      4715      4725
  AlaProLeuGlyHisAspPheCysAlaIleSerLeuSerAspAsnLeuLysProTrpGluValIleThrArgArg
  GCGCCGCTCGGTCATGATTTCTGTGCGATCTCGCTTTCCGACAATCTGAAGCCCTGGGAAGTCATCACCCGGCGT
4740      4750      4760      4770      4780      4790      4800
  LeuArgLeuAlaAlaGluAlaGlyPheValIleAlaLeuTyrAsnProIleSerLysAlaArgProTrpGlnLeu
  CTCAGGCTGGCGGCGGAAGCGGGCTTCGTCATTGCCCTCTACAATCCGATCAGCAAGGCGCGGCCCTGGCAGCTC
4815      4825      4835      4845      4855      4865      4875
  GlyGluAlaPheGluLeuLeuArgSerValLeuProAlaSerValProValIlePheGlyArgAlaAlaGlyArg
  GGTGAGGCCTTCGAGCTTCTGCGCAGCGTTCTGCCGGCAAGCGTTCCGGTCATCTTCGGCCGTGCGGCCGGGCGG
4890      4900      4910      4920      4930      4940      4950
  ProAspGluArgIleAlaValMetProLeuGlyGluAlaAspAlaAsnArgAlaAspMetAlaThrCysValIle
  CCGGACGAACGGATCGCGGTGATGCCGCTCGGCGAGGCCGATGCCAACCGCGCCGACATGGCGACCTGCGTCATC
4965      4975      4985      4995      5005      5015      5025
  IleGlySerProGluThrArgIleValGluArgAspGlyGlnProAspLeuValTyrThrProArgPheTyrAla
  ATCGGCTCGCCGGAGACGCGCATCGTCGAGCGCGACGGCCAACCCGATCTCGTCTACACACCGCGCTTCTATGCA
5040      5050      5060      5070      5080      5090      5100
  GlyAlaSerGln***
  GGGGCGAGCCAGTGA
5115      5125
```

FIG. 16J

COBJ PROTEIN

FIRST RESIDUE = 1
LAST RESIDUE = 254

			NUMBER	NO. %	WEIGHT	WEIGHT %
1	PHE	F	8	3.15	1176.56	4.34
2	LEU	L	20	7.87	2261.60	8.35
3	ILE	I	13	5.12	1470.04	5.43
4	MET	M	7	2.76	917.28	3.39
5	VAL	V	23	9.06	2278.61	8.41
6	SER	S	11	4.33	957.33	3.53
7	PRO	P	18	7.09	1746.90	6.45
8	THR	T	12	4.72	1212.60	4.48
9	ALA	A	40	15.75	2841.60	10.49
10	TYR	Y	7	2.76	1141.42	4.21
11	*	*	0	0.00	0.00	0.00
12	HIS	H	1	0.39	137.06	0.51
13	GLN	Q	7	2.76	896.42	3.31
14	ASN	N	5	1.97	570.20	2.11
15	LYS	K	6	2.36	768.54	2.84
16	ASP	D	13	5.12	1495.39	5.52
17	GLU	E	16	6.30	2064.64	7.62
18	CYS	C	4	1.57	412.04	1.52
19	TRP	W	3	1.18	558.24	2.06
20	ARG	R	19	7.48	2965.90	10.95
21	GLY	G	21	8.27	1197.42	4.42
22	-	-	0	0.00	0.00	0.00

RESIDUES = 254
MOLECULAR WEIGHT = 27088.
INDEX OF POLARITY (%) = 35.
ISOELECTRIC POINT = 5.43
OD 260 (1 mg/ml) = 0.575 OD 260 (1 mg/ml) = 0.922

COBJ FROM 1 TO 254

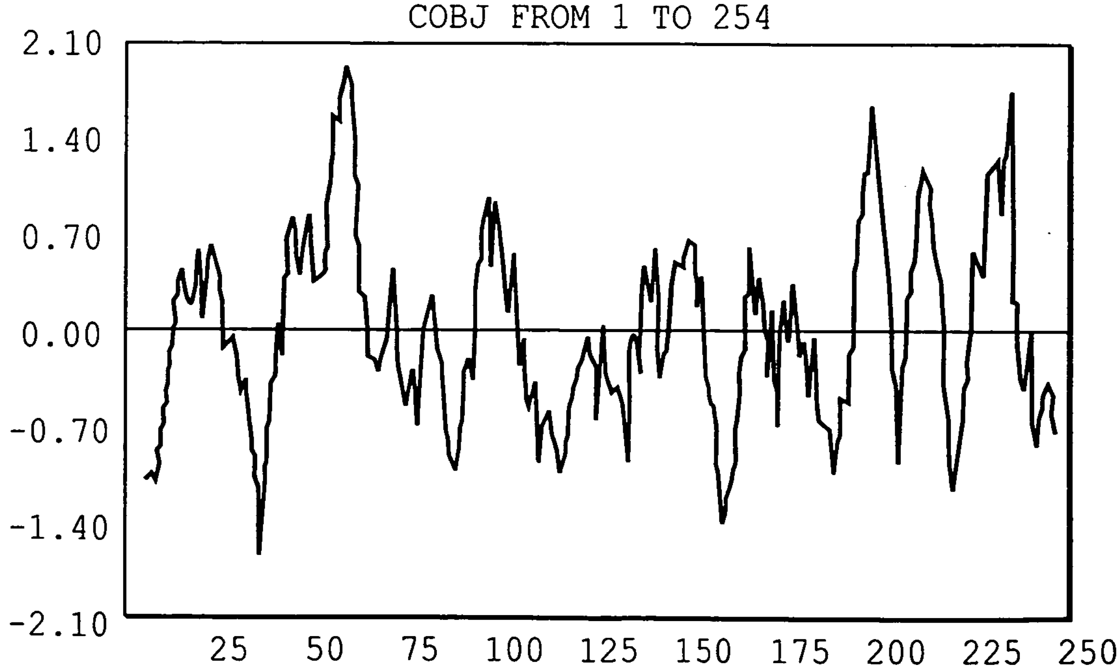


FIG. 16K

<u>cobK</u> GENE (SEQ ID NO: 23) AND COBK PROTEIN (SEQ ID NO: 24)
SEQUENCE OF THE 8753-BP ECORI-ECORI FRAGMENT FROM 2861 TO 3646 ON
THE COMPLEMENTARY STRAND

```
  M  A  G  S  L  F  D  T  S  A  M  E  K  P  R  I  L  I  L  G  G  T  T  E  A
 ATGGCGGGTTCGCTGTTCGACACGTCAGCCATGGAAAAACCTCGTATTCTGATTCTGGGTGGCACCACCGAGGCA
2861      2871      2881      2891      2901      2911      2921      2931
  R  E  L  A  R  R  L  A  E  D  V  R  Y  D  T  A  I  S  L  A  G  R  T  A  D
 CGCGAACTCGCGCGCCGCTTGGCCGAAGATGTCCGCTACGACACCGCCATCTCGCTGGCCGGCCGCACCGCGGAC
2936      2946      2956      2966      2976      2986      2996      3006
  P  R  P  Q  P  V  K  T  R  I  G  G  F  G  G  A  D  G  L  A  H  F  V  H  D
 CCGCGGCCGCAGCCGGTCAAGACGCGCATCGGCGGCTTTGGCGGCGCCGATGGGCTGGCGCATTTCGTGCATGAC
3011      3021      3031      3041      3051      3061      3071      3081
  E  N  I  A  L  L  V  D  A  T  H  P  F  A  A  R  I  S  H  N  A  A  D  A  A
 GAAAACATCGCGCTGCTGGTCGATGCGACGCACCCCTTTGCCGCACGCATTTCGCACAACGCCGCGGACGCAGCG
3086      3096      3106      3116      3126      3136      3146      3156
  Q  R  T  G  V  A  L  I  A  L  R  R  P  E  W  V  P  L  P  G  D  R  W  T  A
 CAAAGAACCGGCGTTGCGCTTATCGCCCTCCGCCGACCGGAATGGGTGCCCCTGCCTGGCGACCGCTGGACTGCT
3161      3171      3181      3191      3201      3211      3221      3231
  V  D  S  V  V  E  A  V  S  A  L  G  D  R  R  R  R  V  F  L  A  I  G  R  Q
 GTCGATAGCGTTGTCGAGGCCGTCAGCGCGCTCGGTGATCGGCGACGCCGCGTCTTCCTGGCGATAGGTCGACAG
3236      3246      3256      3266      3276      3286      3296      3306
  E  A  F  H  F  E  V  A  P  Q  H  S  Y  V  I  R  S  V  D  P  V  T  P  P  L
 GAAGCTTTCCACTTCGAGGTCGCGCCGCAGCACAGCTACGTCATCCGCAGCGTCGATCCGGTGACGCCGCCGCTT
3311      3321      3331      3341      3351      3361      3371      3381
  N  L  P  D  Q  E  A  I  L  A  T  G  P  F  A  E  A  D  E  A  A  L  L  R  S
 AATCTGCCCGACCAGGAGGCGATCCTGGCGACCGGTCCCTTTGCGGAAGCCGACGAAGCCGCGTTGCTCAGGAGT
3386      3396      3406      3416      3426      3436      3446      3456
  R  Q  I  D  V  I  V  A  K  N  S  G  G  S  A  T  Y  G  K  I  A  A  A  R  R
 CGGCAGATCGATGTGATCGTCGCCAAGAACAGCGGTGGCAGCGCCACCTACGGCAAGATTGCCGCAGCGCGCCGG
3461      3471      3481      3491      3501      3511      3521      3531
  L  G  I  E  V  I  M  V  E  R  R  K  P  A  D  V  P  T  V  G  S  C  D  E  A
 CTCGGCATCGAGGTGATCATGGTCGAGCGGCGCAAGCCCGCGGACGTGCCGACGGTCGGCAGTTGCGACGAGGCA
3536      3546      3556      3566      3576      3586      3596      3606
  L  N  R  I  A  H  W  L  A  P  A
 CTCAACCGCATCGCTCACTGGCTCGCCCCTGCATGA
3611      3621      3631      3641
```

FIG. 16L

NAME = COBK

FIRST RESIDUE = 1
LAST RESIDUE = 261

			NUMBER	NO. %	WEIGHT	WEIGHT %
1	PHE	F	8	3.07	1176.55	4.19
2	LEU	L	22	8.43	2487.85	8.86
3	ILE	I	16	6.13	1809.34	6.44
4	MET	M	3	1.15	393.12	1.40
5	VAL	V	21	8.05	2080.44	7.41
6	SER	S	12	4.60	1044.38	3.72
7	PRO	P	17	6.51	1649.90	5.88
8	THR	T	13	4.98	1313.62	4.68
9	ALA	A	42	16.09	2983.56	10.63
10	TYR	Y	3	1.15	489.19	1.74
11	*	*	0	0.00	0.00	0.00
12	HIS	H	7	2.68	959.41	3.42
13	GLN	Q	6	2.30	768.35	2.74
14	ASN	N	5	1.92	570.21	2.03
15	LYS	K	5	1.92	640.47	2.28
16	ASP	D	17	6.51	1955.46	6.96
17	GLU	E	15	5.75	1935.64	6.89
18	CYS	C	1	0.38	103.01	0.37
19	TRP	W	3	1.15	558.24	1.99
20	ARG	R	26	9.96	4058.63	14.45
21	GLY	G	19	7.28	1083.41	3.86
22	-	-	0	0.00	0.00	0.00

RESIDUES = 261
MOLECULAR WEIGHT (MONOISOTOPIC) = 28078.7988
MOLECULAR WEIGHT (AVERAGE) = 28096.0195
INDEX OF POLARITY (%) = 40.64
ISOELECTRIC POINT = 7.54
OD 260 (1mg/ml) = 0.509 OD 280 (1mg/ml) = 0.721

HYDROPHILICITY PROFILE OF THE COBK PROTIEN
FROM 1 TO 261

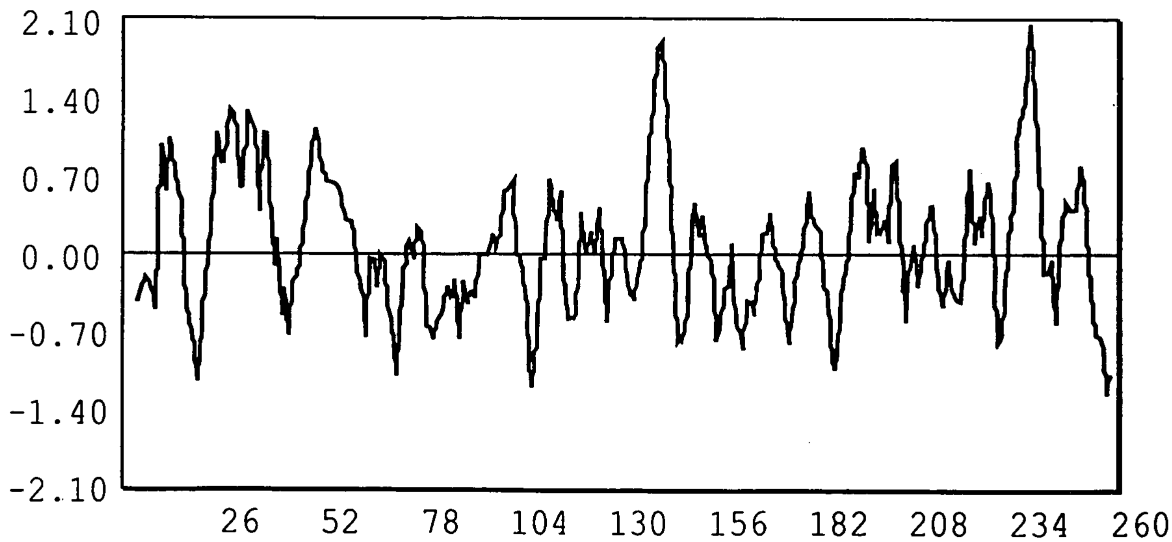


FIG. 16M

<u>cobL</u> GENE (SEQ ID NO: 25) AND COBL PROTEIN (SEQ ID NO: 26)
SEQUENCE OF THE 8753-BP FRAGMENT FROM 5862 TO 7103

```
     MetAlaAspValSerAsnSerGluProAlaIleValSerProTrpLeuThrValIleGlyIleGlyGluAspGly
     ATGGCTGACGTGTCGAACAGCGAACCCGCCATAGTCTCCCCCTGGCTGACCGTCATCGGTATCGGTGAGGATGGT
5862      5872      5882      5892      5902      5912      5922
     ValAlaGlyLeuGlyAspGluAlaLysArgLeuIleAlaGluAlaProValValTyrGlyGlyHisArgHisLeu
     GTAGCGGGTCTCGGCGACGAGGCCAAGCGGCTGATCGCCGAAGCGCCGGTCGTCTACGGCGGCCATCGTCATCTG
5937      5947      5957      5967      5977      5987      5997
     GluLeuAlaAlaSerLeuIleThrGlyGluAlaHisAsnTrpLeuSerProLeuGluArgSerValValGluIle
     GAGCTCGCCGCCTCCCTCATCACCGGCGAAGCGCACAATTGGCTAAGCCCCCTCGAACGCTCGGTCGTCGAGATC
6012      6022      6032      6042      6052      6062      6072
     ValAlaArgArgGlySerProValValValLeuAlaSerGlyAspProPhePhePheGlyValGlyValThrLeu
     GTCGCGCGTCGCGGCAGCCCGGTGGTGGTGCTTGCCTCGGGCGACCCGTTCTTCTTCGGCGTCGGCGTGACGCTG
6087      6097      6107      6117      6127      6137      6147
     AlaArgArgIleAlaSerAlaGluIleArgThrLeuProAlaProSerSerIleSerLeuAlaAlaSerArgLeu
     GCGCGCCGCATCGCCTCGGCCGAAATACGCACGCTTCCGGCGCCGTCGTCGATCAGTCTTGCCGCCTCGCGCCTC
6162      6172      6182      6192      6202      6212      6222
     GlyTrpAlaLeuGlnAspAlaThrLeuValSerValHisGlyArgProLeuAspLeuValArgProHisLeuHis
     GGCTGGGCGCTGCAGGATGCGACGCTCGTCTCCGTACATGGGCGGCCGCTGGATCTGGTGCGACCGCATTTGCAT
6237      6247      6257      6267      6277      6287      6297
     ProGlyAlaArgValLeuThrLeuThrSerAspGlyAlaGlyProArgAspLeuAlaGluLeuLeuValSerSer
     CCGGGGGCGCGTGTGCTTACGCTCACGTCGGACGGTGCGGGTCCGCGAGACCTTGCCGAGCTTCTGGTTTCAAGC
6312      6322      6332      6342      6352      6362      6372
     GlyPheGlyGlnSerArgLeuThrValLeuGluAlaLeuGlyGlyAlaGlyGluArgValThrThrGlnIleAla
     GGCTTCGGTCAGTCGCGACTGACCGTGCTCGAAGCGCTGGGCGGCGCCGGCGAACGGGTGACGACGCAGATCGCC
6387      6397      6407      6417      6427      6437      6447
     AlaArgPheMetLeuGlyLeuValHisProLeuAsnValCysAlaIleGluValAlaAlaAspGluGlyAlaArg
     GCGCGCTTCATGCTCGGCCTCGTGCATCCTTTGAACGTCTGCGCCATTGAGGTGGCGGCCGACGAGGGCGCGCGC
6462      6472      6482      6492      6502      6512      6522
     IleLeuProLeuAlaAlaGlyArgAspAspAlaLeuPheGluHisAspGlyGlnIleThrLysArgGluValArg
     ATCCTGCCGCTTGCCGCCGGCCGCGACGATGCGCTGTTCGAACATGACGGGCAGATCACCAAGCGCGAGGTGCGG
6537      6547      6557      6567      6577      6587      6597
     AlaLeuThrLeuSerAlaLeuAlaProArgLysGlyGluLeuLeuTrpAspIleGlyGlyGlySerGlySerIle
     GCGCTGACGCTGTCGGCACTCGCACCGCGCAAGGGCGAACTGCTATGGGACATCGGCGGCGGCTCCGGCTCGATC
6612      6622      6632      6642      6652      6662      6672
     GlyIleGluTrpMetLeuAlaAspProThrMetGlnAlaIleThrIleGluValGluProGluArgAlaAlaArg
     GGCATCGAATGGATGCTCGCCGATCCGACCATGCAGGCGATCACCATCGAGGTTGAGCCGGAGCGGGCAGCGCGC
6687      6697      6707      6717      6727      6737      6747
```

FIG. 16N

```
   IleGlyArgAsnAlaThrMetPheGlyValProGlyLeuThrValValGluGlyGluAlaProAlaAlaLeuAla
   ATCGGCCGCAACGCGACGATGTTCGGCGTGCCCGGGCTGACGGTTGTCGAAGGCGAGGCGCCGGCGGCGCTTGCC
6762      6772      6782      6792      6802      6812      6822
   GlyLeuProGlnProAspAlaIlePheIleGlyGlyGlyGlySerGluAspGlyValMetGluAlaAlaIleGlu
   GGCCTGCCACAACCGGACGCGATCTTCATCGGCGGCGGCGGCAGCGAAGACGGCGTCATGGAAGCAGCGATCGAG
6837      6847      6857      6867      6877      6887      6897
   AlaLeuLysSerGlyGlyArgLeuValAlaAsnAlaValThrThrAspMetGluAlaValLeuLeuAspHisHis
   GCGCTCAAGTCAGGCGGACGGCTGGTTGCCAACGCGGTGACGACGGACATGGAAGCGGTGCTGCTCGATCATCAC
6912      6922      6932      6942      6952      6962      6972
   AlaArgLeuGlyGlySerLeuIleArgIleAspIleAlaArgAlaGlyProIleGlyGlyMetThrGlyTrpLys
   GCGCGGCTCGGCGGTTCGCTGATCCGCATCGATATCGCGCGTGCAGGACCCATCGGCGGCATGACCGGCTGGAAG
6987      6997      7007      7017      7027      7037      7047
   ProAlaMetProValThrGlnTrpSerTrpThrLysGly***
   CCGGCCATGCCGGTCACCCAATGGTCGTGGACGAAGGGCTAA
7062      7072      7082      7092      7102
```

FIG. 16O

COBL PROTEIN

FIRST RESIDUE = 1
LAST RESIDUE = 413

			NUMBER	NO. %	WEIGHT	WEIGHT %
1	PHE	F	8	1.94	1176.56	2.74
2	LEU	L	47	11.38	5314.76	12.39
3	ILE	I	26	6.30	2940.08	6.85
4	MET	M	9	2.18	1179.36	2.75
5	VAL	V	34	8.23	3368.38	7.85
6	SER	S	25	6.05	2175.75	5.07
7	PRO	P	24	5.81	2329.20	5.43
8	THR	T	21	5.08	2122.05	4.95
9	ALA	A	56	13.56	3978.24	9.27
10	TYR	Y	1	0.24	163.06	0.38
11	*	*	0	0.00	0.00	0.00
12	HIS	H	10	2.42	1370.60	3.19
13	GLN	Q	7	1.69	896.42	2.09
14	ASN	N	5	1.21	570.20	1.33
15	LYS	K	6	1.45	768.54	1.79
16	ASP	D	19	4.60	2185.57	5.09
17	GLU	E	27	6.54	3484.08	8.12
18	CYS	C	1	0.24	103.01	0.24
19	TRP	W	8	1.94	1488.64	3.47
20	ARG	R	28	6.78	4370.80	10.19
21	GLY	G	51	12.35	2908.02	6.78
22	-	-	0	0.00	0.00	0.00

RESIDUES = 413
MOLECULAR WEIGHT = 42911.
INDEX OF POLARITY (%) = 36.
ISOELECTRIC POINT = 5.70
OD 260 (1mg/ml) = 0.754 OD 280 (1mg/ml) = 1.064

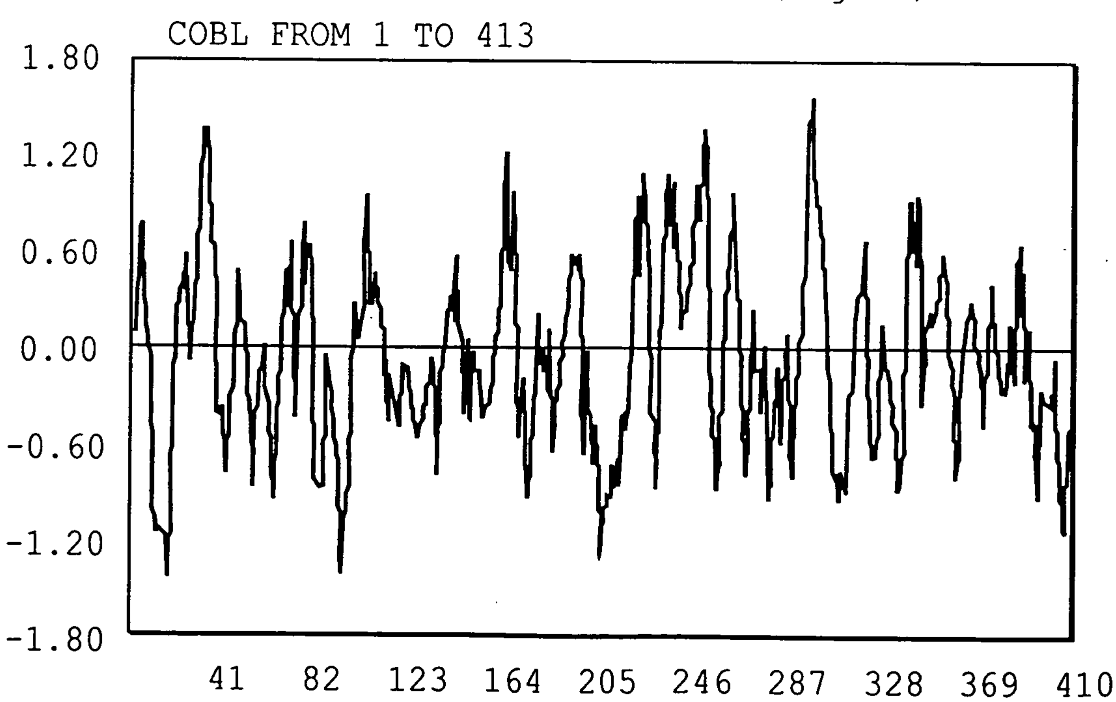


FIG. 16P

cobM GENE (SEQ ID NO: 27) AND COBM PROTEIN (SEQ ID NO: 28)
SEQUENCE OF THE 8753-BP FRAGMENT FROM 7172 TO 7930

```
  MetThrValHisPheIleGlyAlaGlyProGlyAlaAlaAspLeuIleThrValArgGlyArgAspLeuIleGly
  ATGACGGTACATTTCATCGGCGCCGGCCCGGGAGCCGCAGACCTGATCACGGTGCGTGGTCGCGACCTGATCGGG
7172      7182      7192      7202      7212      7222      7232
  ArgCysProValCysLeuTyrAlaGlySerIleValSerProGluLeuLeuArgTyrCysProProGlyAlaArg
  CGCTGCCCGGTCTGCCTTTACGCCGGCTCGATCGTCTCGCCGGAGCTGCTGCGATATTGCCCGCCGGGCGCCCGC
7247      7257      7267      7277      7287      7297      7307
  IleValAspThrAlaProMetSerLeuAspGluIleGluAlaGluTyrValLysAlaGluAlaGluGlyLeuAsp
  ATTGTCGATACGGCGCCGATGTCCCTCGACGAGATCGAGGCGGAGTATGTGAAGGCCGAAGCCGAAGGGCTCGAC
7322      7332      7342      7352      7362      7372      7382
  ValAlaArgLeuHisSerGlyAspLeuSerValTrpSerAlaValAlaGluGlnIleArgArgLeuGluLysHis
  GTGGCGCGGCTTCATTCGGGCGACCTTTCGGTCTGGAGTGCTGTGGCCGAACAGATCCGCCGGCTCGAGAAGCAT
7397      7407      7417      7427      7437      7447      7457
  GlyIleAlaTyrThrMetThrProGlyValProSerPheAlaAlaAlaAlaSerAlaLeuGlyArgGluLeuThr
  GGCATCGCCTATACGATGACGCCGGGCGTTCCTTCCTTTGCGGCGGCGGCTTCAGCGCTCGGTCGCGAATTGACC
7472      7482      7492      7502      7512      7522      7532
  IleProAlaValAlaGlnSerLeuValLeuThrArgValSerGlyArgAlaSerProMetProAsnSerGluThr
  ATTCCGGCCGTGGCCCAGAGCCTGGTGCTGACCCGCGTTTCGGGCCGCGCCTCGCCGATGCCGAACTCAGAAACG
7547      7557      7567      7577      7587      7597      7607
  LeuSerAlaPheGlyAlaThrGlySerThrLeuAlaIleHisLeuAlaIleHisAlaLeuGlnGlnValValGlu
  CTTTCCGCTTTCGGCGCTACGGGATCGACGCTGGCAATCCACCTTGCGATCCATGCGCTTCAGCAGGTGGTCGAG
7622      7632      7642      7652      7662      7672      7682
  GluLeuThrProLeuTyrGlyAlaAspCysProValAlaIleValValLysAlaSerTrpProAspGluArgVal
  GAACTGACGCCGCTCTACGGTGCCGACTGCCCGGTCGCCATCGTCGTCAAGGCCTCCTGGCCGGACGAACGCGTG
7697      7707      7717      7727      7737      7747      7757
  ValArgGlyThrLeuGlyAspIleAlaAlaLysValAlaGluGluProIleGluArgThrAlaLeuIlePheVal
  GTGCGCGGCACGCTCGGTGACATCGCCGCCAAGGTGGCGGAAGAGCCGATCGAGCGCACGGCGCTGATCTTCGTC
7772      7782      7792      7802      7812      7822      7832
  GlyProGlyLeuGluAlaSerAspPheArgGluSerSerLeuTyrAspProAlaTyrGlnArgArgPheArgGly
  GGTCCGGGGCTCGAAGCCTCCGATTTCCGTGAAAGCTCGCTCTACGATCCCGCCTATCAGCGGCGCTTCAGAGGG
7847      7857      7867      7877      7887      7897      7907
  ArgGlyGlu
  CGCGGCGAA
7922      7932      7942      7952      7962      7972      7982
```

FIG. 16Q

COBM PROTEIN

FIRST RESIDUE = 1
LAST RESIDUE = 253

			NUMBER	NO. %	WEIGHT	WEIGHT %
1	PHE	F	6	2.37	882.42	3.29
2	LEU	L	24	9.49	2713.92	10.11
3	ILE	I	15	5.93	1696.20	6.32
4	MET	M	4	1.58	524.16	1.95
5	VAL	V	22	8.70	2179.54	8.12
6	SER	S	18	7.11	1566.54	5.84
7	PRO	P	17	6.72	1649.85	6.15
8	THR	T	13	5.14	1313.65	4.89
9	ALA	A	35	13.83	2486.40	9.26
10	TYR	Y	7	2.77	1141.42	4.25
11	*	*	0	0.00	0.00	0.00
12	HIS	H	5	1.98	685.30	2.55
13	GLN	Q	5	1.98	640.30	2.39
14	ASN	N	1	0.40	114.04	0.42
15	LYS	K	4	1.58	512.36	1.91
16	ASP	D	11	4.35	1265.33	4.71
17	GLU	E	19	7.51	2451.76	9.13
18	CYS	C	4	1.58	412.04	1.53
19	TRP	W	2	0.79	372.16	1.39
20	ARG	R	19	7.51	2965.90	11.05
21	GLY	G	22	8.70	1254.44	4.67
22	-	-	0	0.00	0.00	0.00

RESIDUES = 253
MOLECULAR WEIGHT = 26846.
INDEX OF POLARITY (%) = 38.
ISOELECTRIC POINT = 5.58
OD 260 (1mg/ml) = 0.461 OD 280 (1mg/ml) = 0.724

COBM FROM 1 TO 253

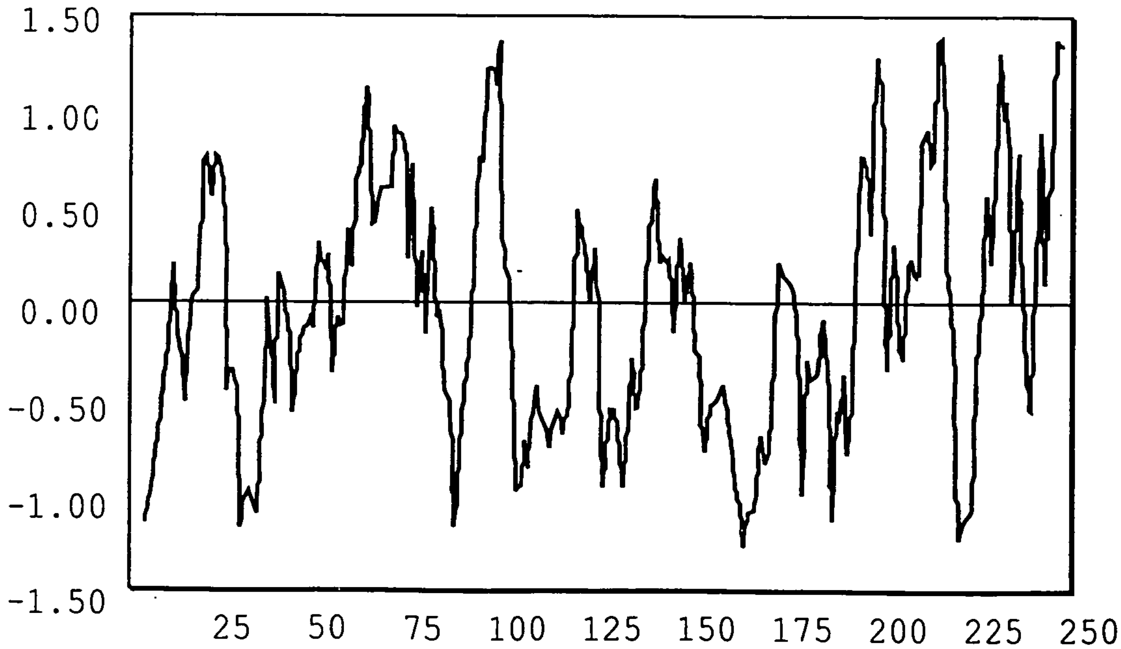
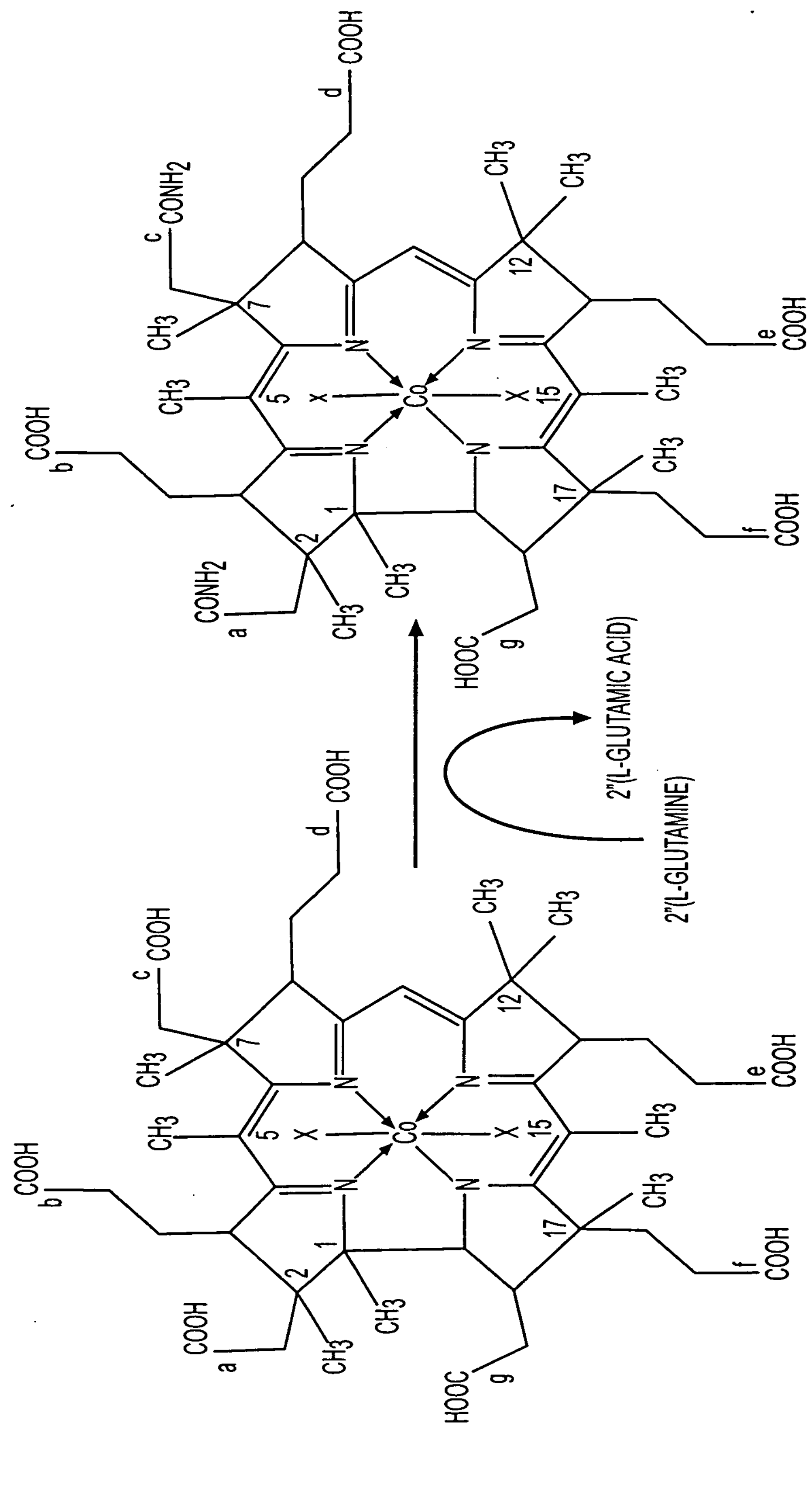


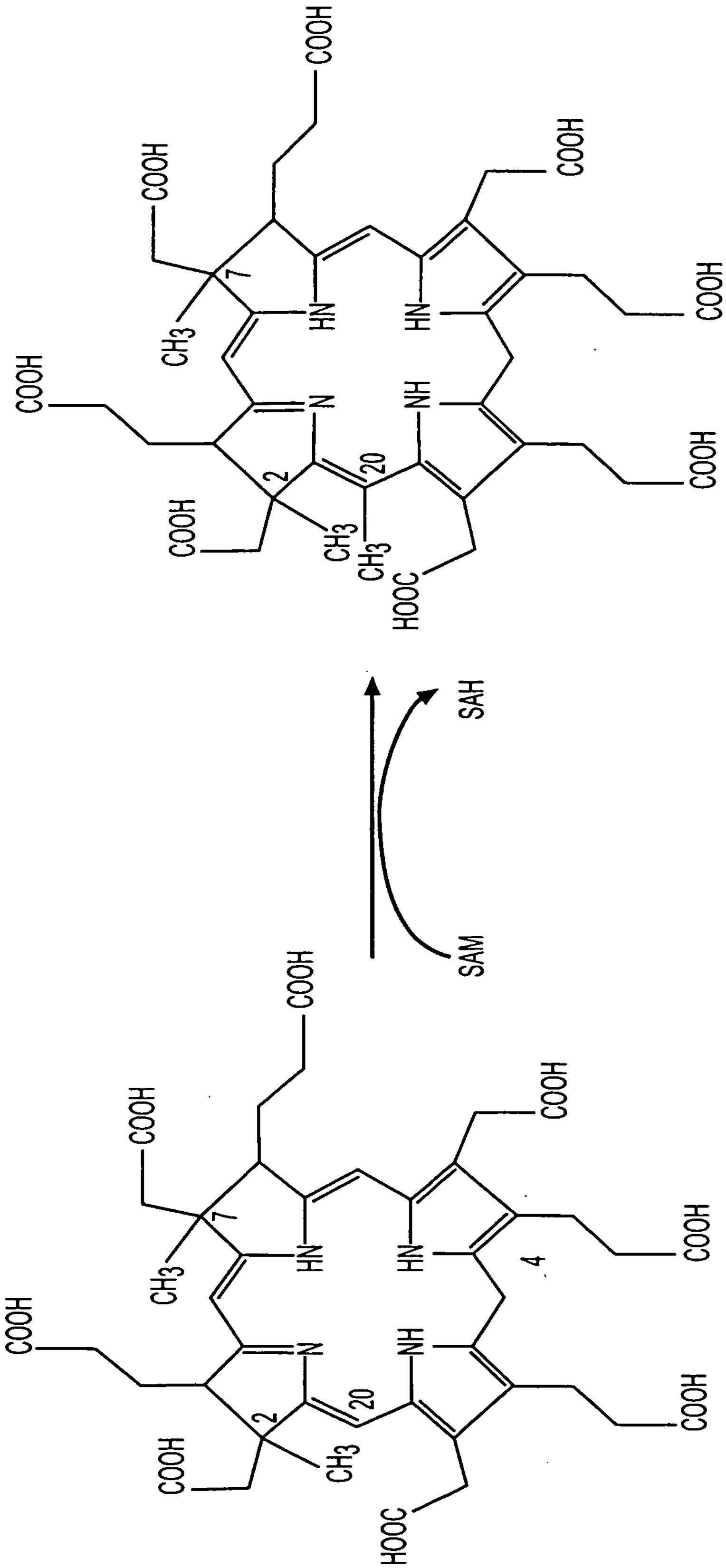
FIG. 16R



COBYRINIC ACID

COBYRINIC ACID DIAMIDE

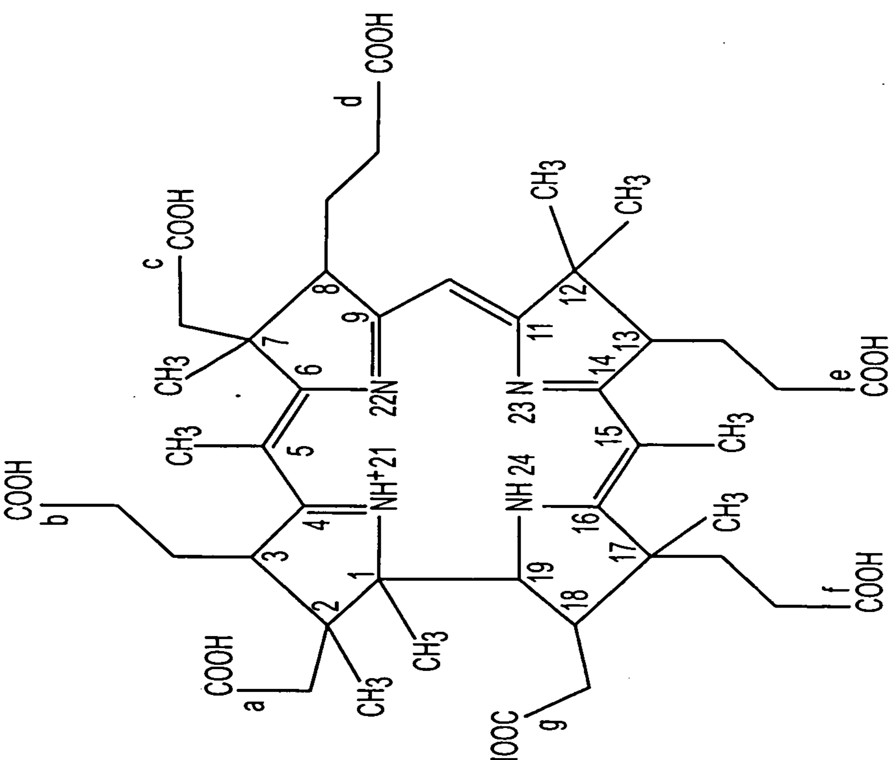
FIG. 17



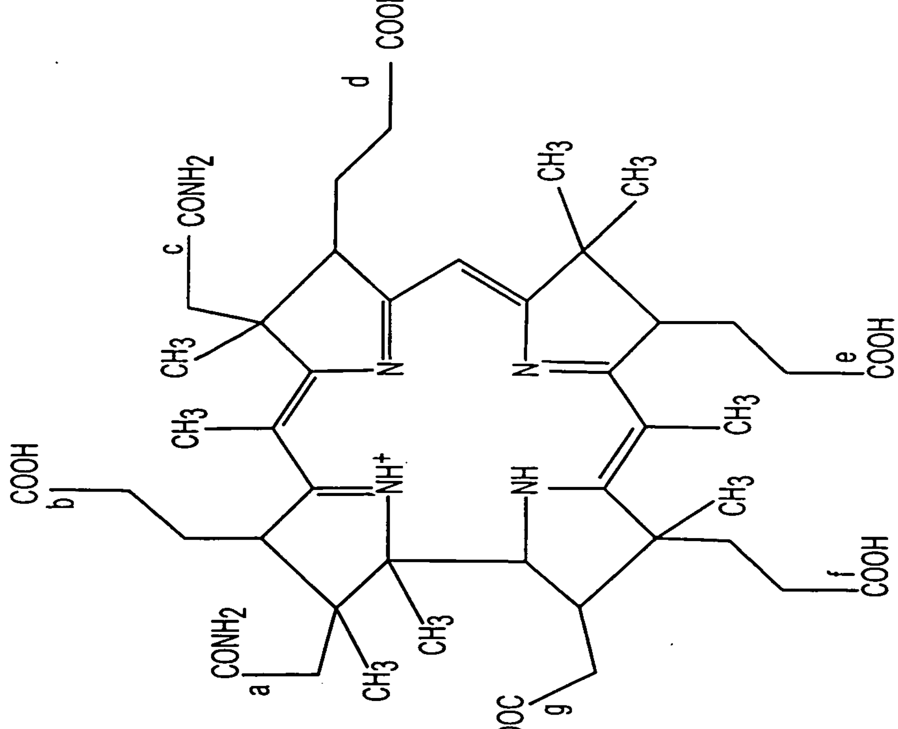
PRECORRIN-2

PRECORRIN-3

FIG. 18



HYDROGENOBYRINIC ACID



HYDROGENOBYRINIC ACID DIAMIDE

FIG. 19

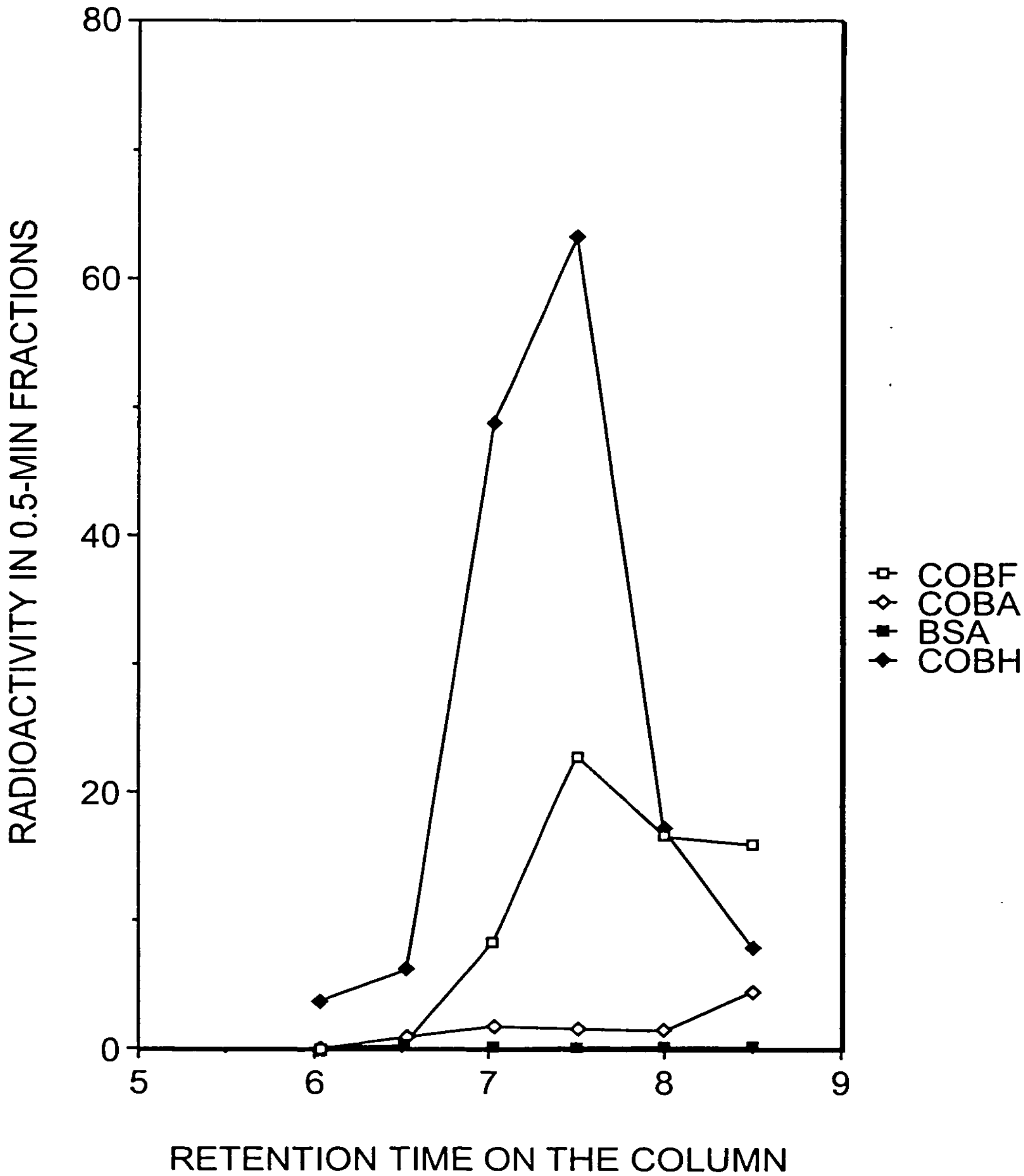

80
60
40
20
0
5
6
7
8
9
RADIOACTIVITY IN 0.5-MIN FRACTIONS
RETENTION TIME ON THE COLUMN
COBF
COBA
BSA
COBH

FIG. 20

```
      10         20        30        40
COBA  LPALEKGSVWL-VGAGPGDPGLLTLHAANALRQADVIVH -(AMINO ACIDS 10-46 AND 88-157 OF SEQ ID NO:4)
      - --  = - - ==-===== ===- =  == ====-
COBI  VSGVGVGRL-IGVGTGPGDPELLTVKAVKALGQADVLAY -(AMINO ACIDS 6-44 AND 99-164 OF SEQ ID NO:20)
         10        20        30        40
      ________________________________________
                     REGION 1

     90       100       110       120       130       140       150
COBA LARAGNRVLRLKGGDPFVFGRGGEEALTLVEHQVPFRIVPGITAGIGGLAYAGIPVTHREVNHAVTFLTG
     == ==  =  =  ===  -=         - = -   =  --=====  =  - ==-=-      -  -- = =
COBI LA-AGRTVAVLSEGDPLFYGSYMHLHVRLANR-FPVEVIPGITAMSGCWSLAGLPLVQ-G-DDVLSVLPG
              110       120        130       140       150         160
     _____________________              ___________________
          REGION 2                           REGION 3
```

FIG. 21

```
ALIGNMENT BETWEEN THE PROTEINS COBA OF PSEUDOMONAS DENITRIFICANS
AND CYSG OF ESCHERICHIA COLI
COBA SEQUENCE
CYSG SEQUENCE
                                   1
       10        20        30        40        50        60        70
DDLFAGLPALEKGSVWLVGAGPGDPGLLTLHAANALRQADVIVHDALVNEDCLKLARPGAVLEFAGKRGG
--=    =   -= = ======== ===== - - - ====-= = == -= - = =  =   = ===-=
EQLINE-PLDHRGEVVLVGAGPGDAGLLTLKGLQQIQQADVVVYDRLVSDDIMNLVRRDADRVFVGKRAG
      210       220       230       240       250       260       270
       80        90       100  2    110       120       130       140
KPSPKQRDISLRLVELARAGNRVLRLKGGDPFVFGRGGEEALTLVEHQVPFRIVPGITAGIGGLAYAGIP
    = -=    =-  =  = ==-========-=======  ==  -   -== -======- =  ==-===   3
YHCVPQEEINQILLREAQKGKRVVRLKGGDPFIFGRGGEELETLCNAGIPFSVVPGITAASGCSAYSGIP
      280       290       300       310       320       330       340
      150       160       170       180       190       200       210
VTHREVNHAVTFLTGHDSSGLVPDRINWQGIASGSPVIVMYMAMKHIGAITANLIAGGRSPDEPVAFVCN
3 -====-  -=  -===  -=   - --=- -=-     -= ==--    --=    ==  =    - === = =
LTHRDYAQSVRLITGHLKTG-G-E-LDWENLAAEKQTLVFYMGLNQAATIQQKLIEHGMPGEMPVAIVEN
      350       360          370       380       390       400
      220       230       240       250
AATPQQAVLETTLARAEADVAAAGLEPPAIVVVGEVVRLRAALDWIG
---  = =---==-    ---=    -- =-----= == ==  =-= -
GTAVTQRVIDGTLTQL-GELAQQ-MNSPSLIIIGRVVGLRDKLNWFS
          420       430       440       450
```

COBA SEQUENCE FROM 3 TO 259 -(AMINO ACIDS 3-259 OF SEQ ID NO:4)
CYSG SEQUENCE FROM 204 TO 460 -(SEQ ID NO:55)
STRICT HOMOLOGY OF AMINO ACIDS; 41.6%

FIG. 22

REGION 1

```
CYSG(209-248) EPLDHRGEVVLVGAGPGDAGLLTLKGLQQIQQADVVVYDR
COBA(9-48)    LPALEKGSVWLVGAGPGDPGLLTLHAANALRQADVIVHDA
COBI(1-40)    VSGVGVGRLIGVGTGPGDPELLTVKAVKALGQADVLAYFA
COBF(1-40)    MAEAGMRKILIIGIGSGNPEHMTVQAINALNCADVLFIPT
COBJ(1-40)    MTGTLYVVGTGPGSAKQMTPETAEAVAAAQEFYGYFPYLD
COBL(6-45)    NSEPAIVSPWLTVIGIGEDGVAGLGDEAKALIAEAPVVYG
COBM(1-34)          MTVHFIGAGPGAADLITVRGRDLIGRCPVCLYAG
```

REGION 2

```
CYSG(288-310) EAQKGKRVVRLKGGDPFIFGRGG-(CYSG IS SEQ ID NO:55)
COBA(88-110)  LARAGNRVLRLKGGDPFVFGRGG-(COBA IS SEQ ID NO:4)
COBI(98-120)  HLAAGRTVAVLSEGDPLFYGSYM-(COBI IS SEQ ID NO:20)
COBF(60-83)   VTRKDSRTVEFAVPVRRTEGVSY-(COBF IS SEQ ID NO:14)
COBJ(68-80)   RAAAGVXVCMVSGGDPGVFAMAA-(COBJ IS SEQ ID NO:22)
COBL(76-98)   VARRGSPVVVLASGDPFFFGVGV-(COBL IS SEQ ID NO:26)
COBM(69-91)   AEAEGLDVARLHSGDLSVWSAVA-(COBM IS SEQ ID NO:28)
```

REGION 3

```
CYSG(325-342) VVPGITAASGCSAYSGIP
COBA(125-142) IVPGITAGIGGLAYAGIP
COBI(134-151) VIPGITAMSGCWSLAGLP
COBF(85-102)  SVDDWHAQIAGIYEALLS
COBJ(110-127) ITPGVTAMLAVAARIGAP
COBL(154-171) RVLTLTSDGAGPRDLAEL
COBM(102-119) IAYTMTPGVPSFAAAASA
```

(AMINO ACID NOS. LISTED CORRESPOND TO IDENTIFIED AMINO ACIDS OF SEQ ID NOS.)

FIG. 23

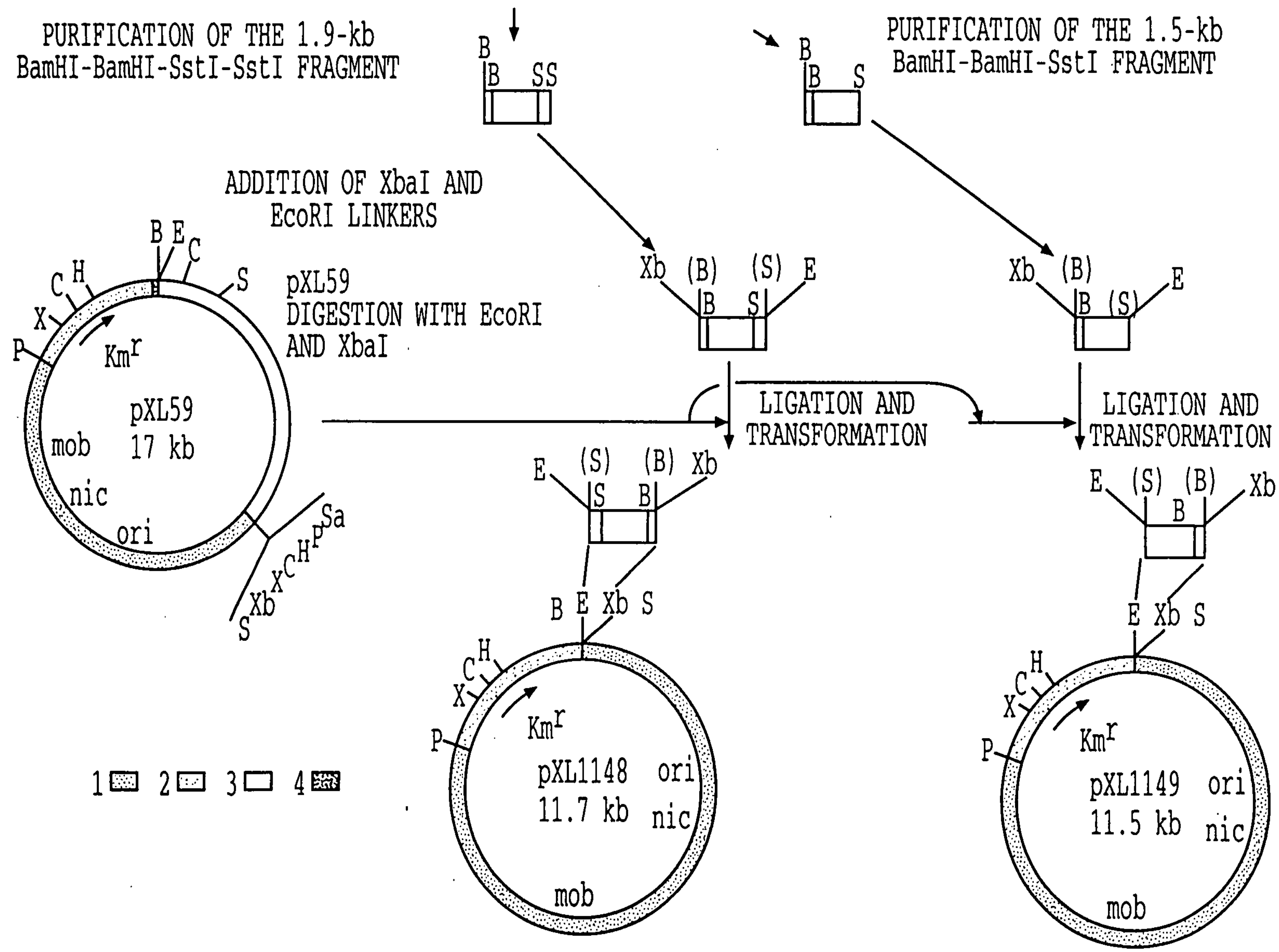

PURIFICATION OF THE 1.9-kb
BamHI-BamHI-SstI-SstI FRAGMENT
PURIFICATION OF THE 1.5-kb
BamHI-BamHI-SstI FRAGMENT
ADDITION OF XbaI AND
EcoRI LINKERS
pXL59
DIGESTION WITH EcoRI
AND XbaI
pXL59
17 kb
Km^r
mob
nic
ori
LIGATION AND
TRANSFORMATION
LIGATION AND
TRANSFORMATION
pXL1148
11.7 kb
ori
nic
mob
pXL1149
11.5 kb
ori
nic
mob
1
2
3
4

FIG. 24

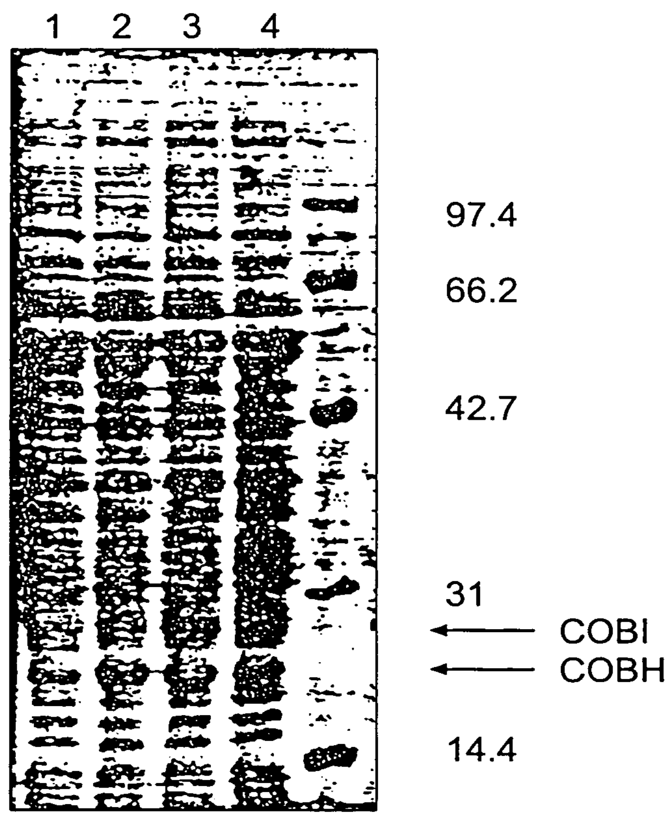


FIG. 25

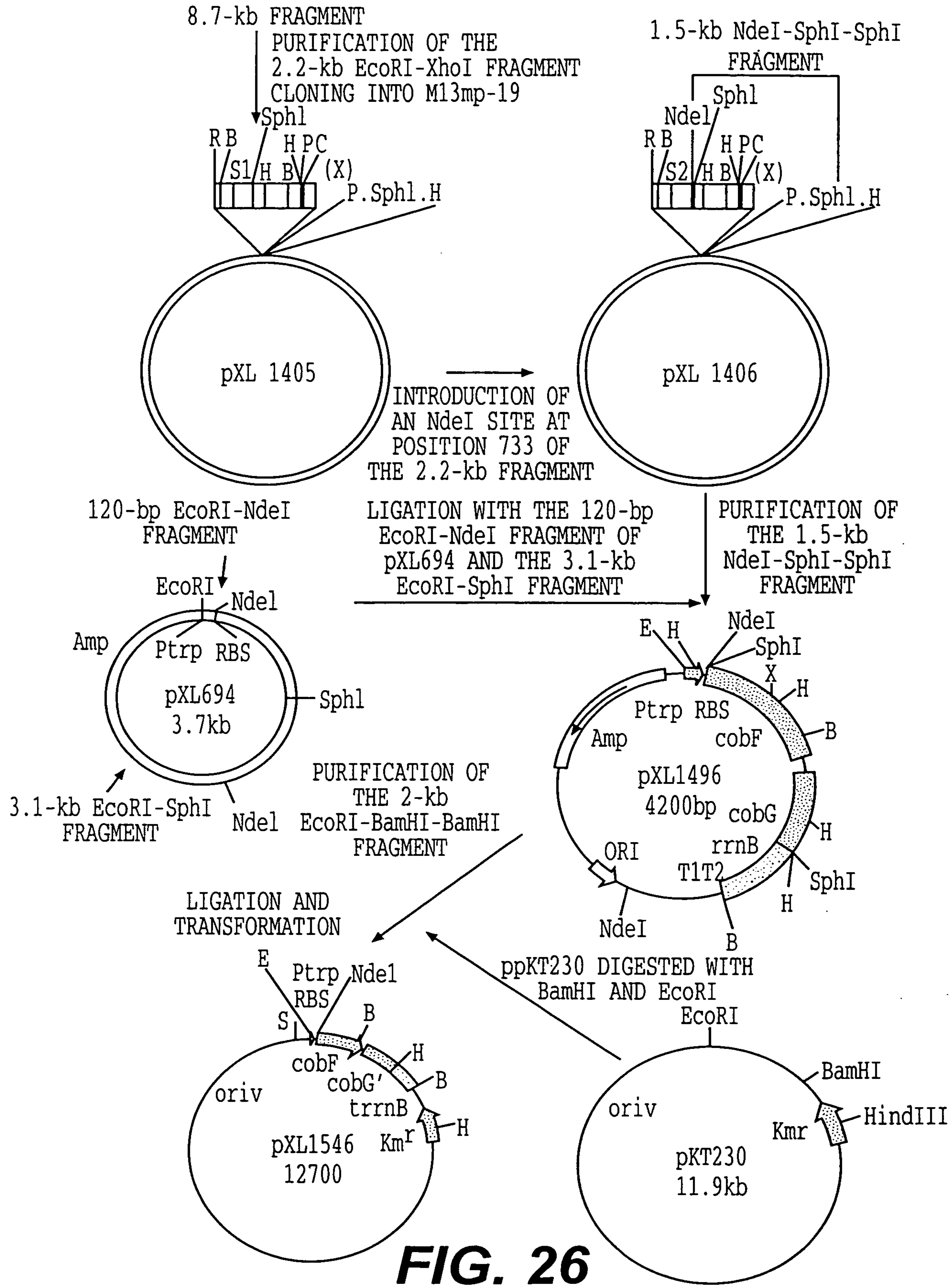

8.7-kb FRAGMENT
PURIFICATION OF THE 2.2-kb EcoRI-XhoI FRAGMENT CLONING INTO M13mp-19
Sphl
R B S1 H B H P C (X)
P.Sphl.H
pXL 1405
1.5-kb NdeI-SphI-SphI FRAGMENT
Ndel Sphl
R B S2 H B H P C (X)
P.Sphl.H
pXL 1406
INTRODUCTION OF AN NdeI SITE AT POSITION 733 OF THE 2.2-kb FRAGMENT
120-bp EcoRI-NdeI FRAGMENT
EcoRI
Ndel
Amp
Ptrp RBS
pXL694
3.7kb
Sphl
3.1-kb EcoRI-SphI FRAGMENT
Ndel
LIGATION WITH THE 120-bp EcoRI-NdeI FRAGMENT OF pXL694 AND THE 3.1-kb EcoRI-SphI FRAGMENT
PURIFICATION OF THE 1.5-kb NdeI-SphI-SphI FRAGMENT
E H
NdeI
SphI
X
H
Ptrp RBS
Amp
cobF
B
pXL1496
4200bp
cobG
H
ORI
rrnB
T1T2
SphI
H
NdeI
B
PURIFICATION OF THE 2-kb EcoRI-BamHI-BamHI FRAGMENT
LIGATION AND TRANSFORMATION
ppKT230 DIGESTED WITH BamHI AND EcoRI
E
Ptrp
RBS
Ndel
S
B
cobF
H
cobG'
B
oriv
trrnB
H
pXL1546
12700
Km^r
EcoRI
BamHI
oriv
Kmr
HindIII
pKT230
11.9kb

FIG. 26

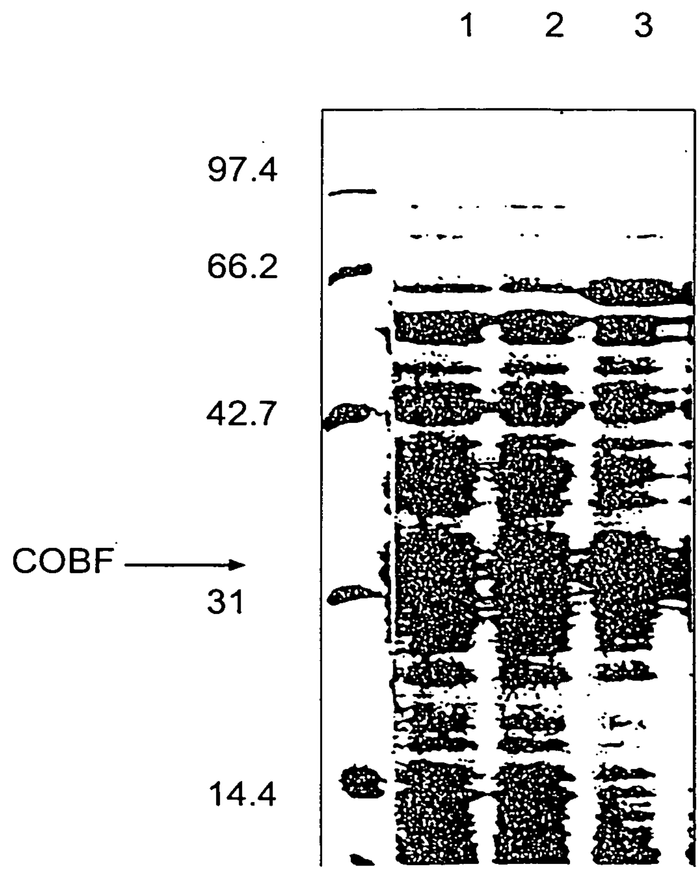


FIG. 27

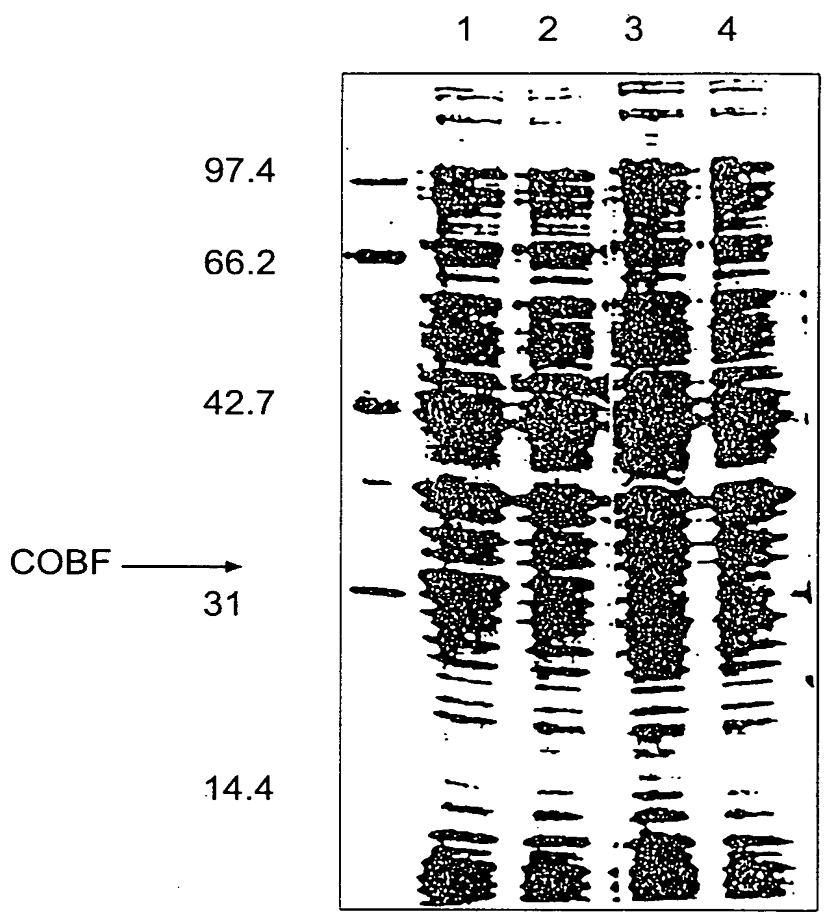


FIG. 28

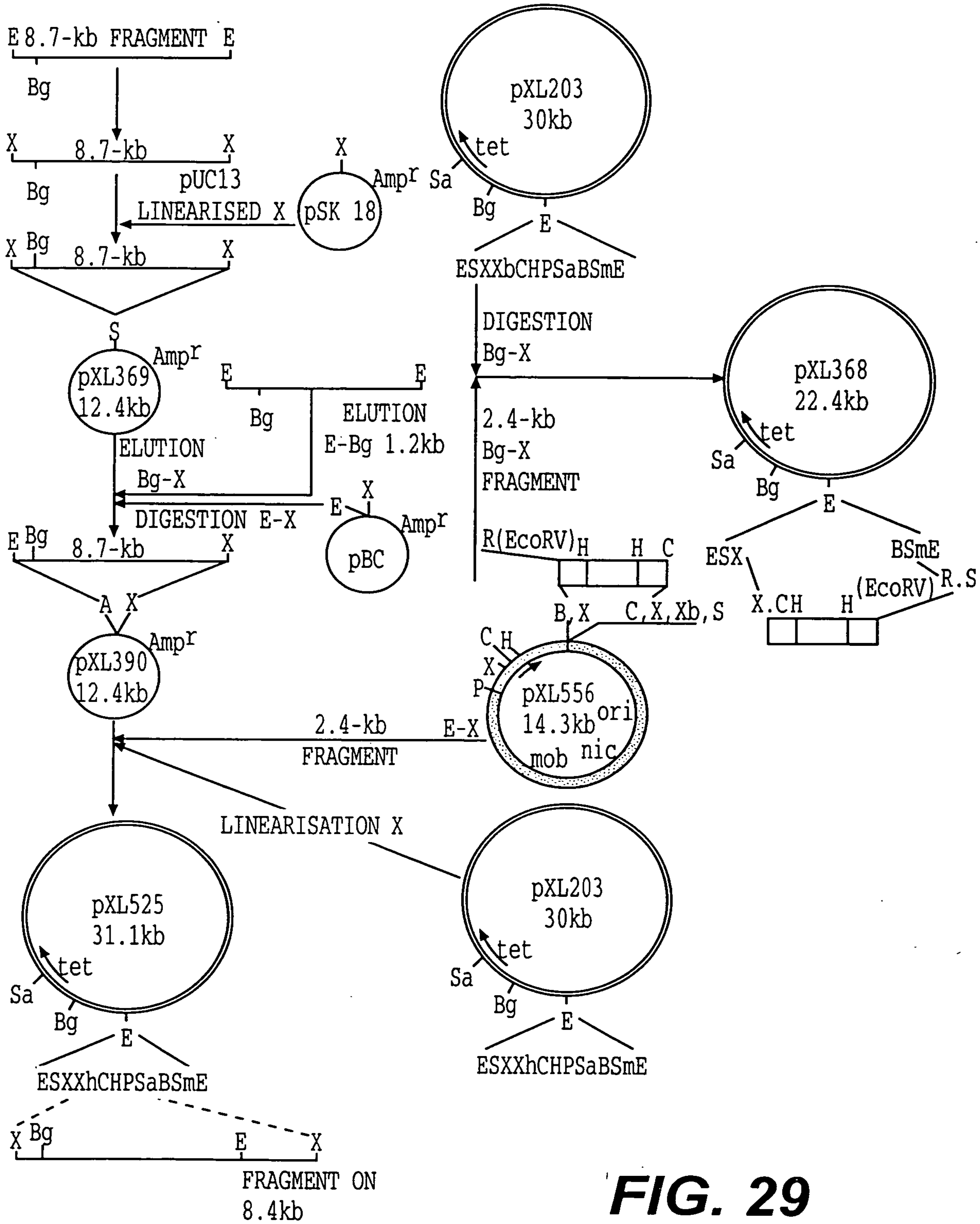

E 8.7-kb FRAGMENT E
Bg
X 8.7-kb X
Bg
pUC13
LINEARISED X
pSK 18
X
Ampr
pXL203
30kb
tet
Sa
Bg
E
ESXXbCHPSaBSmE
DIGESTION
Bg-X
2.4-kb
Bg-X
FRAGMENT
pXL368
22.4kb
S
pXL369
12.4kb
Ampr
E E
Bg
ELUTION
E-Bg 1.2kb
ELUTION
Bg-X
DIGESTION E-X
pBC
8.7-kb
A X
pXL390
12.4kb
R(EcoRV) H H C
B,X C,X,Xb,S
ESX
BSmE
X.CH H (EcoRV) R.S
pXL556
14.3kb
ori
mob
nic
2.4-kb
FRAGMENT
E-X
LINEARISATION X
pXL525
31.1kb
ESXXhCHPSaBSmE
FRAGMENT ON
8.4kb

FIG. 29

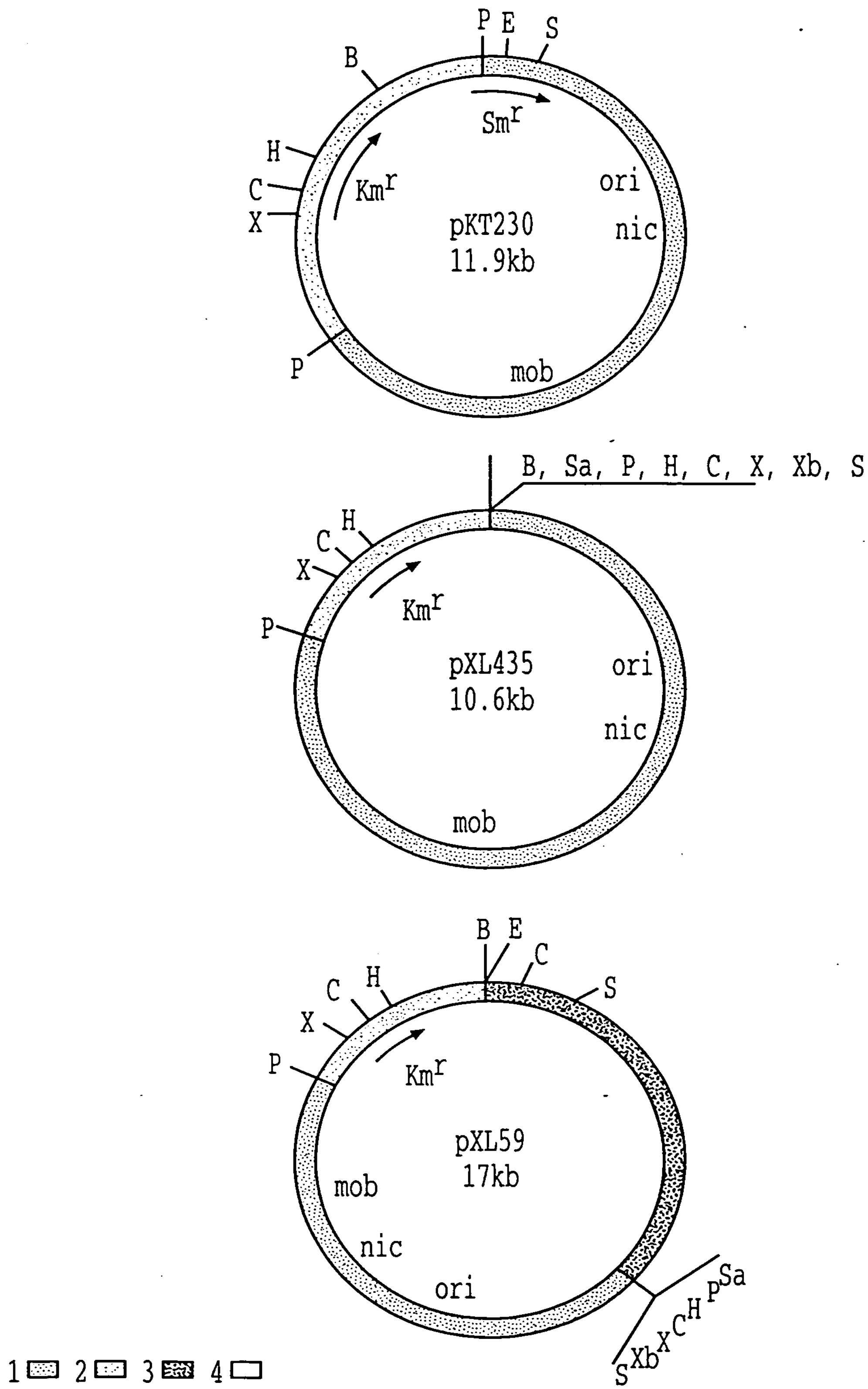

P E S
B
Sm^r
H
C
X
Km^r
ori
pKT230
11.9kb
nic
P
mob
B, Sa, P, H, C, X, Xb, S
H
C
X
Km^r
P
pXL435
10.6kb
ori
nic
mob
B E
C
C H
S
X
P
Km^r
pXL59
17kb
mob
nic
ori
S Xb X C H P Sa
1 2 3 4

FIG. 30

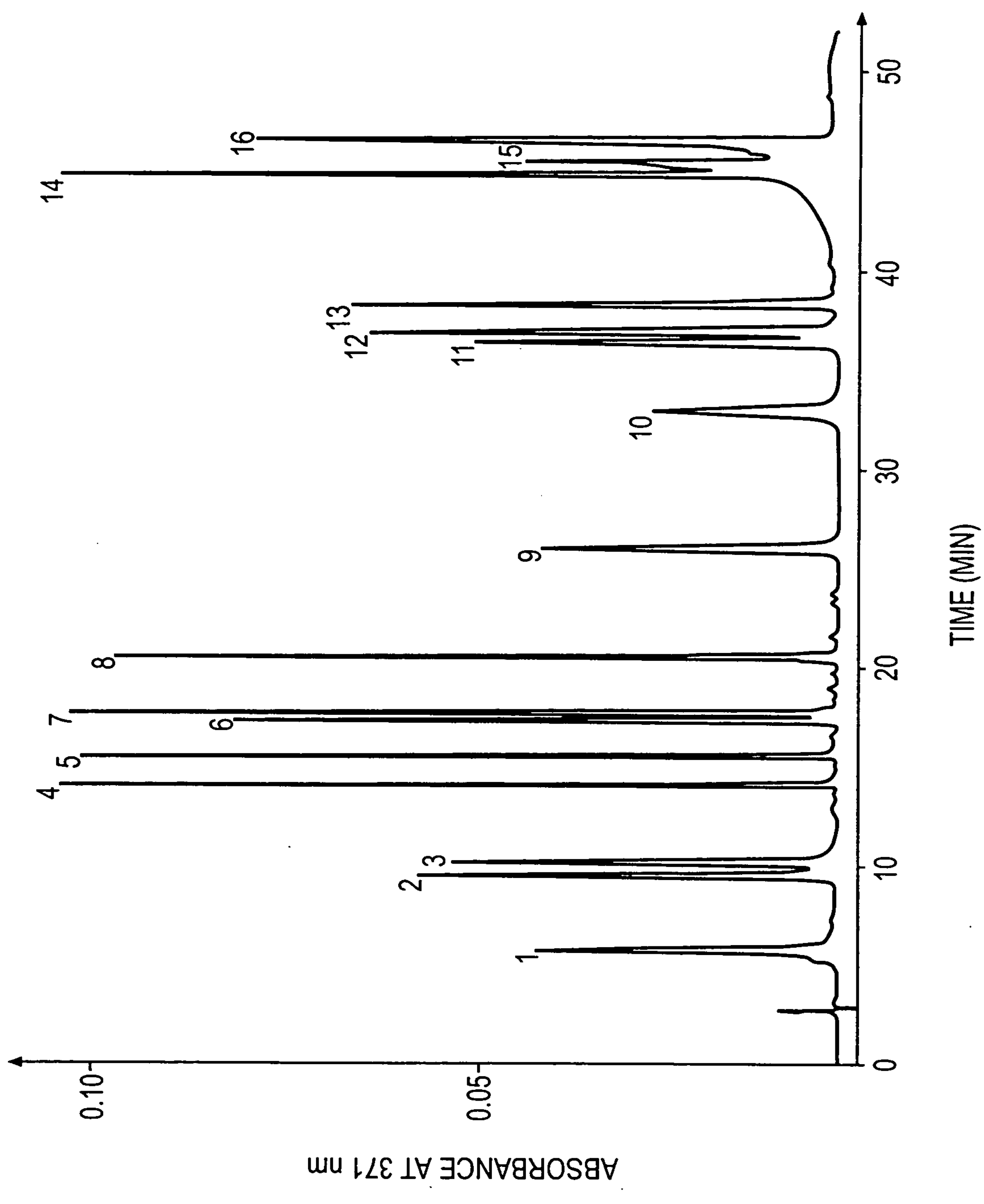

ABSORBANCE AT 371 nm
0.10
0.05
TIME (MIN)
0
10
20
30
40
50
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16

FIG. 31

```
        10         20         30         40         50         60
GTCGACGAGT ATGGTCAGGT TCAGGGTCTG GTGACGCTGG AGGACATTCT GGAGGAGATC
CAGCTGCTCA TACCAGTCCA AGTCCCAGAC CACTGCGACC TCCTGTAAGA CCTCCTCTAG

        70         80         90        100        110        120
GTCGGCGATA TCGCCGATGA GCACGACCTC GACATTCAGG GCGTGCGCCA GGAAGCCGAT
CAGCCGCTAT AGCGGCTACT CGTGCTGGAG CTGTAAGTCC CGCACGCGGT CCTTCGGCTA

       130        140        150        160        170        180
GGCTCGATCG TCGTCGATGG CTCGGTGCCG ATCCGCGATC TCAACCGCGC GCTCGACTGG
CCGAGCTAGC AGCAGCTACC GAGCCACGGC TAGGCGCTAG AGTTGGCGCG CGAGCTGACC

       190        200        210        220        230        240
TCGCTGCCGG ACGAGGAGGC GACGACGGTG GCCGGTCTGG TCATCCACGA GTCCAAGAGC
AGCGACGGCC TGCTCCTCCG CTGCTGCCAC CGGCCAGACC AGTAGGTGCT CAGGTTCTCG

       250        260        270        280        290        300
ATTCCGGAGG AGCGCCAGGC CTTCACCTTC CACGGCAAAC GCTTCATCGT GATGAAGCGG
TAAGGCCTCC TCGCGGTCCG GAAGTGGAAG GTGCCGTTTG CGAAGTAGCA CTACTTCGCC

       310        320        330        340        350        360
GTGAAGAACC GCATTACCAA GCTGCGCATC CGTCCGGCGG AAGAGGGTGC TCCGCCGGCG
CACTTCTTGG CGTAATGGTT CGACGCGTAG GCAGGCCGCC TTCTCCCACG AGGCGGCCGC

       370        380        390        400        410        420
TGATGGCCGC GATTGCCTCT ACCAGCGGGT CGGCTCGCCG GGGGCTGCCG GCTCGACGGC
ACTACCGGCG CTAACGGAGA TGGTCGCCCA GCCGAGCGGC CCCCGACGGC CGAGCTGCCG

       430        440        450        460        470        480
GAGCGCATGC AGGCCGGCGT CGAGTTCTGG CTTCAGGAGA TCATTGATGG CGCGGTGGCG
CTCGCGTACG TCCGGCCGCA GCTCAAGACC GAAGTCCTCT AGTAACTACC GCGCCACCGC

       490        500        510        520        530        540
GGCGACACGG CTCATGCCGG CAAAGGCGCT AGAAACGATA CGCACCCGCA TGTGGGACTC
CCGCTGTGCC GAGTACGGCC GTTTCCGCGA TCTTTGCTAT GCGTGGGCGT ACACCCTGAG

       550        560        570        580        590        600
GCCGGTACCA TCGAAGCCCG GCTGATGGCC GGTATGCTGA TGGCTCTCGT TGATGACCTC
CGGCCATGGT AGCTTCGGGC CGACTACCGG CCATACGACT ACCGAGAGCA ACTACTGGAG
```

FIG. 32A

610 620 630 640 650 660
GAGCCGTTCA GGGTGGAAGG CCTCGATCAG CTTCTTTTCG ATGGTCTCGG TGAGCGACAT
CTCGGCAAGT CCCACCTTCC GGAGCTAGTC GAAGAAAAGC TACCAGAGCC ACTCGCTGTA

670 680 690 700 710 720
TCTTCCGTCC CATTTTGCTG TTTGCTTGGC GCCCCCTCGC AGTTAAGAAC CCGGTAATCG
AGAAGGCAGG GTAAAACGAC AAACGAACCG CGGGGGAGCG TCAATTCTTG GGCCATTAGC

730 740 750 760 770 780
CTGGCACGGC GGCGCAAAAT GCCCGCACAA AGCCAGCAAC ATTCCGCTTT GTCAATTCTT
GACCGTGCCG CCGCGTTTTA CGGGCGTGTT TCGGTCGTTG TAAGGCGAAA CAGTTAAGAA

790 800 810 820 830 840
GTTGTGACTC CCGCCAAACC CCATAATGAG CGCCATGAGA CTCGATTCAA AATACTTCGA
CAACACTGAG GGCGGTTTGG GGTATTACTC GCGGTACTCT GAGCTAAGTT TTATGAAGCT

850 860 870 880 890 900
TCGCATTCGA ACCCGGCGCA AGGTCGAGCC GCAGCAGAGC CGGCGGCTCC CGTCTGTCAG
AGCGTAAGCT TGGGCCGCGT TCCAGCTCGG CGTCGTCTCG GCCGCCGAGG GCAGACAGTC

910 920 930 940 950 960
TGGGACGGCT GCGATCAGAA GGGTGTGCAC CGGGCGCCCG TCGGTCGCAA CGCCGAGGGG
ACCCTGCCGA CGCTAGTCTT CCCACACGTG GCCCGCGGGC AGCCAGCGTT GCGGCTCCCC

970 980 990 1000 1010 1020
CAGTACTTCA TGTTCTGCTT CGAGCACGTG AAGGAATACA ACAAGGGCTA CAACTTCTTC
GTCATGAAGT ACAAGACGAA GCTCGTGCAC TTCCTTATGT TGTTCCCGAT GTTGAAGAAG

1030 1040 1050 1060 1070 1080
TCCGGCCTCT CCGACAGCGA GGTCGCCCGC TACCAGAAGG AAGCGATCAC CGGTCATCGG
AGGCCGGAGA GGCTGTCGCT CCAGCGGGCG ATGGTCTTCC TTCGCTAGTG GCCAGTAGCC

1090 1100 1110 1120 1130 1140
CCCACCTGGA CCGTCGGCGT CAACAAGAAC GCCAAGAACG GCCCGACCCA GTCGCAGACG
GGGTGGACCT GGCAGCCGCA GTTGTTCTTG CGGTTCTTGC CGGGCTGGGT CAGCGTCTGC

1150 1160 1170 1180 1190 1200
CGGTCTGGCT CTGCCGGCGC CCAGGCCCGC ATGCGCGATC CCTTCGGCTT TGTCAGCGAG
GCCAGACCGA GACGGCCGCG GGTCCGGGCG TACGCGCTAG GGAAGCCGAA ACAGTCGCTC

FIG. 32B

```
      1210       1220       1230       1240       1250       1260
GCGCGGGCGC GATCCGGTCG TCCCGAGCCA CGCCAGCGCA AGCTGAAGAC GCTCGAGGCG
CGCGCCCGCG CTAGGCCAGC AGGGCTCGGT GCGGTCGCGT TCGACTTCTG CGAGCTCCGC

      1270       1280       1290       1300       1310       1320
AAGGCCTTCG AAACGCTTGG TCTCGGAGCC TCGGCGACCA CTGCCGACAT CAAGGCGGCC
TTCCGGAAGC TTTGCGAACC AGAGCCTCGG AGCCGCTGGT GACGGCTGTA GTTCCGCCGG

      1330       1340       1350       1360       1370       1380
TACAAGGACC TCGTCAAGAA GCATCACCCC GATGCCAATG GCGGAGATAG AGGATCGGAA
ATGTTCCTGG AGCAGTTCTT CGTAGTGGGG CTACGGTTAC CGCCTCTATC TCCTAGCCTT

      1390       1400       1410       1420       1430       1440
GAGCGTTTTC GCGCGGTTAT TCAGGCCTAC CAATTGTTAA AACAGGCTGG TTTCTGCTAA
CTCGCAAAAG CGCGCCAATA AGTCCGGATG GTTAACAATT TTGTCCGACC AAAGACGATT

      1450       1460       1470       1480       1490       1500
CAACCCGGAT TAATACAGAA GCACTTTTGC AGGCGAATGC GCGGGTGCCG TCCGGTGGCC
GTTGGGCCTA ATTATGTCTT CGTGAAAACG TCCGCTTACG CGCCCACGGC AGGCCACCGG

      1510       1520       1530       1540       1550       1560
GCTCTGGAGA CATGATGAGC AAGATTGACC TCGACATTTC CAACCTCCCC GACACCACGA
CGAGACCTCT GTACTACTCG TTCTAACTGG AGCTGTAAAG GTTGGAGGGG CTGTGGTGCT

      1570       1580       1590       1600       1610       1620
TTTCCGTCCG GGAGGTTTTC GGTATTGATA CGGATTTGCG CGTTCCTGCC TATTCGAAGG
AAAGGCAGGC CCTCCAAAAG CCATAACTAT GCCTAAACGC GCAAGGACGG ATAAGCTTCC

      1630       1640       1650       1660       1670       1680
GCGACGCCTA TGTCCCGGAT CTGGATCCGG ACTACCTCTT CGACCGCGAA ACGACGCTCG
CGCTGCGGAT ACAGGGCCTA GACCTAGGCC TGATGGAGAA GCTGGCGCTT TGCTGCGAGC

      1690       1700       1710       1720       1730       1740
CCATTCTCGC AGGCTTCGCC CACAACCGAC GCGTGATGGT GTCGGGCTAT CACGGCACCG
GGTAAGAGCG TCCGAAGCGG GTGTTGGCTG CGCACTACCA CAGCCCGATA GTGCCGTGGC

      1750       1760       1770       1780       1790       1800
GCAAGTCCAC CCATATCGAG CAGGTCGCCG CGCGCCTCAA CTGGCCGTGC GTGCGCGTCA
CGTTCAGGTG GGTATAGCTC GTCCAGCGGC GCGCGGAGTT GACCGGCACG CACGCGCAGT
```

FIG. 32C

```
      1810       1820       1830       1840       1850       1860
ACCTCGATAG CCATGTCAGC CGTATCGACC TCGTCGGCAA GGACGCGATC GTCGTCAAGG
TGGAGCTATC GGTACAGTCG GCATAGCTGG AGCAGCCGTT CCTGCGCTAG CAGCAGTTCC

      1870       1880       1890       1900       1910       1920
ACGGCCTGCA GGTCACCGAA TTCAAGGACG GCATCCTGCC CTGGGCCTAC CAGCACAATG
TGCCGGACGT CCAGTGGCTT AAGTTCCTGC CGTAGGACGG GACCCGGATG GTCGTGTTAC

      1930       1940       1950       1960       1970       1980
TCGCGCTCGT CTTCGACGAA TACGATGCCG GCCGCCCGGA CGTCATGTTC GTCATCCAGC
AGCGCGAGCA GAAGCTGCTT ATGCTACGGC CGGCGGGCCT GCAGTACAAG CAGTAGGTCG

      1990       2000       2010       2020       2030       2040
GCGTGCTGGA ATCCTCCGGC CGCCTGACGC TGCTCGACCA GAGCCGTGTC ATCCGTCCGC
CGCACGACCT TAGGAGGCCG GCGGACTGCG ACGAGCTGGT CTCGGCACAG TAGGCAGGCG

      2050       2060       2070       2080       2090       2100
ACCCGGCCTT CCGCCTGTTT GCGACCGCCA ACACCGTCGG CCTCGGCGAC ACGACCGGCC
TGGGCCGGAA GGCGGACAAA CGCTGGCGGT TGTGGCAGCC GGAGCCGCTG TGCTGGCCGG

      2110       2120       2130       2140       2150       2160
TCTATCACGG CACGCAGCAG ATCAACCAGG CGCAGATGGA CCGCTGGTCG ATCGTCACCA
AGATAGTGCC GTGCGTCGTC TAGTTGGTCC GCGTCTACCT GGCGACCAGC TAGCAGTGGT

      2170       2180       2190       2200       2210       2220
CGCTGAACTA CCTGCCGCAC GACAAGGAAG TCGACATCGT CGCCGCCAAG GTCAAGGGCT
GCGACTTGAT GGACGGCGTG CTGTTCCTTC AGCTGTAGCA GCGGCGGTTC CAGTTCCCGA

      2230       2240       2250       2260       2270       2280
TCACCGCCGA CAAGGGCCGC GAGACCGTCT CCAAGATGGT ACGTGTCGCC GACCTCACGC
AGTGGCGGCT GTTCCCGGCG CTCTGGCAGA GGTTCTACCA TGCACAGCGG CTGGAGTGCG

      2290       2300       2310       2320       2330       2340
GCGCAGCCTT CATCAATGGC GATCTCTCGA CTGTCATGAG CCCGCGTACG GTCATCACCT
CGCGTCGGAA GTAGTTACCG CTAGAGAGCT GACAGTACTC GGGCGCATGC CAGTAGTGGA

      2350       2360       2370       2380       2390       2400
GGGCCGAGAA CGCCCACATC TTCGGCGACA TCGCTTTCGC CTTCCGCGTG ACCTTCCTCA
CCCGGCTCTT GCGGGTGTAG AAGCCGCTGT AGCGAAAGCG GAAGGCGCAC TGGAAGGAGT
```

FIG. 32D

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      2410       2420       2430       2440       2450       2460
ACAAGTGCGA CGAGCTGGAG CGGGCGCTGG TCGCCGAGCA CTACCAGCGC GCCTTCGGCA
TGTTCACGCT GCTCGACCTC GCCCGCGACC AGCGGCTCGT GATGGTCGCG CGGAAGCCGT

      2470       2480       2490       2500       2510       2520
TCGAGCTGAA GGAATGCGCT GCCAACATCG TGCTCGAAGC CACCGCCTGA TCCCACGGCC
AGCTCGACTT CCTTACGCGA CGGTTGTAGC ACGAGCTTCG GTGGCGGACT AGGGTGCCGG

      2530       2540       2550       2560       2570       2580
TGCCGTCCCC TTTGGGAGGG CGGGTCATGA CGCTGTGGCA AACCGGATGA CGCCCCACTG
ACGGCAGGGG AAACCCTCCC GCCCAGTACT GCGACACCGT TTGGCCTACT GCGGGGTGAC

      2590       2600       2610       2620       2630       2640
GGGCGCCGTC GCCTCTGGCT GAAGAAGGAA CTGTCGTGAG CTCGAATTCG AAGGCAAAGC
CCCGCGGCAG CGGAGACCGA CTTCTTCCTT GACAGCACTC GAGCTTAAGC TTCCGTTTCG

      2650       2660       2670       2680       2690       2700
CAACCACGCG CGAGAATGCT GCGGAACCGT TCAAGCGGGC GCTTTCCGGC TGCATCCGAT
GTTGGTGCGC GCTCTTACGA CGCCTTGGCA AGTTCGCCCG CGAAAGGCCG ACGTAGGCTA

      2710       2720       2730       2740       2750       2760
CGATCGCGGG CGATGCCGAG GTGGAAGTCG CCTTCGCCAA CGAGCGGCCG GGCATGACCG
GCTAGCGCCC GCTACGGCTC CACCTTCAGC GGAAGCGGTT GCTCGCCGGC CCGTACTGGC

      2770       2780       2790       2800       2810       2820
GCGAACGCAT CCGTCTGCCG GAACTTTCCA AGCGCCCGAC CCTGCAGGAA CTTGCCGTGA
CGCTTGCGTA GGCAGACGGC CTTGAAAGGT TCGCGGGCTG GGACGTCCTT GAACGGCACT

      2830       2840       2850       2860       2870       2880
CCCGCGGGCT CGGTGACAGC ATGGCGCTGC GCAAGGCCTG TACGCATGCG CGGATCCAGC
GGGCGCCCGA GCCACTGTCG TACCGCGACG CGTTCCGGAC ATGCGTACGC GCCTAGGTCG

      2890       2900       2910       2920       2930       2940
GCACCATGTC GCCGCAAGGG GCGGACGCCC GCGCGATCTT CGATGCGGTG GAGCAGGCTC
CGTGGTACAG CGGCGTTCCC CGCCTGCGGG CGCGCTAGAA GCTACGCCAC CTCGTCCGAG

      2950       2960       2970       2980       2990       3000
GTGTCGAGGC GATCGGGTCG TTGCGCATGG CGGGTGTCGC CAAGAACCTC AACGTCATGC
CACAGCTCCG CTAGCCCAGC AACGCGTACC GCCCACAGCG GTTCTTGGAG TTGCAGTACG
```

FIG. 32E

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      3010       3020       3030       3040       3050       3060
TCGAAGAGAA ATACGCCAAG GCGAATTTCG CAACGATCGA GCGCCAGGCG GACGCGCCGC
AGCTTCTCTT TATGCGGTTC CGCTTAAAGC GTTGCTAGCT CGCGGTCCGC CTGCGCGGCG

      3070       3080       3090       3100       3110       3120
TCGGCGAGGC CGTAGCGCTG CTGGTGCGCG AGAAGCTGAC GGGCCAGAAG CCGCCGGCGT
AGCCGCTCCG GCATCGCGAC GACCACGCGC TCTTCGACTG CCCGGTCTTC GGCGGCCGCA

      3130       3140       3150       3160       3170       3180
CTGCCGGCAA GGTGCTCGAC CTCTGGCGCG AGTTCATCGA GGGCAAGGCT GCCGGCGACA
GACGGCCGTT CCACGAGCTG GAGACCGCGC TCAAGTAGCT CCCGTTCCGA CGGCCGCTGT

      3190       3200       3210       3220       3230       3240
TTGAGCACCT GTCGTCGACG ATCAACAACC AGCAGGCCTT TGCCCGGGTC GTTCGCGACA
AACTCGTGGA CAGCAGCTGC TAGTTGTTGG TCGTCCGGAA ACGGGCCCAG CAAGCGCTGT

      3250       3260       3270       3280       3290       3300
TGCTGACCTC GATGGAAGTC GCCGAGAAAT ACGGTGACGA CGACAACGAG CCGGACGAGC
ACGACTGGAG CTACCTTCAG CGGCTCTTTA TGCCACTGCT GCTGTTGCTC GGCCTGCTCG

      3310       3320       3330       3340       3350       3360
AGGAAAGCGA GACCGACGAA GACCAGCCGC GCAGCCAGGA GCAGGACGAG AACGCCAGCG
TCCTTTCGCT CTGGCTGCTT CTGGTCGGCG CGTCGGTCCT CGTCCTGCTC TTGCGGTCGC

      3370       3380       3390       3400       3410       3420
ACGAGGAAGC CGGCGACGAT GCCGCACCCG CCGACGAGAA CCAGGCTGCC GAAGAGCAGA
TGCTCCTTCG GCCGCTGCTA CGGCGTGGGC GGCTGCTCTT GGTCCGACGG CTTCTCGTCT

      3430       3440       3450       3460       3470       3480
TGGAAGAAGG CGAGATGGAC GGCGCGGAGA TCTCCGACGA CGATCTCCAG GACGAAGGCG
ACCTTCTTCC GCTCTACCTG CCGCGCCTCT AGAGGCTGCT GCTAGAGGTC CTGCTTCCGC

      3490       3500       3510       3520       3530       3540
ACGAGGACAG CGAAACGCCC GGCGAGGTCA AGCGTCCGAA CCAGCCCTTC GCCGACTTCA
TGCTCCTGTC GCTTTGCGGG CCGCTCCAGT TCGCAGGCTT GGTCGGGAAG CGGCTGAAGT

      3550       3560       3570       3580       3590       3600
ACGAGAAGGT CGACTACGCC GTCTTCACCC GCGAGTTCGA CGAGACGATT GCCTCGGAAG
TGCTCTTCCA GCTGATGCGG CAGAAGTGGG CGCTCAAGCT GCTCTGCTAA CGGAGCCTTC
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FIG. 32F

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      3610       3620       3630       3640       3650       3660
AGCTTTGCGA CGAGGCCGAG CTCGACCGGC TGCGCGCCTT CCTCGACAAG CAGCTTGCCC
TCGAAACGCT GCTCCGGCTC GAGCTGGCCG ACGCGCGGAA GGAGCTGTTC GTCGAACGGG

      3670       3680       3690       3700       3710       3720
ATCTTCAAGG CGCGGTCGGC CGCCTTGCCA ACCGGCTGCA GCGCCGCCTG ATGGCGCAGC
TAGAAGTTCC GCGCCAGCCG GCGGAACGGT TGGCCGACGT CGCGGCGGAC TACCGCGTCG

      3730       3740       3750       3760       3770       3780
AGAACCGCTC CTGGGAGTTC GATCTCGAAG AGGGGTATCT CGATTCGGCG CGGCTTCAGC
TCTTGGCGAG GACCCTCAAG CTAGAGCTTC TCCCCATAGA GCTAAGCCGC GCCGAAGTCG

      3790       3800       3810       3820       3830       3840
GCATCATCAT CGATCCGATG CAGCCGCTTT CCTTCAAGCG CGAAAAGGAC ACCAACTTCC
CGTAGTAGTA GCTAGGCTAC GTCGGCGAAA GGAAGTTCGC GCTTTTCCTG TGGTTGAAGG

      3850       3860       3870       3880       3890       3900
GCGATACCGT CGTGACGCTG CTGATCGACA ATTCCGGCTC GATGCGCGGC CGTCCGATCA
CGCTATGGCA GCACTGCGAC GACTAGCTGT TAAGGCCGAG CTACGCGCCG GCAGGCTAGT

      3910       3920       3930       3940       3950       3960
CGGTTGCCGC CACCTGCGCC GATATCCTGG CGCGCACGCT CGAGCGCTGC GGCGTCAAGG
GCCAACGGCG GTGGACGCGG CTATAGGACC GCGCGTGCGA GCTCGCGACG CCGCAGTTCC

      3970       3980       3990       4000       4010       4020
TCGAGATCCT CGGTTTTACC ACCAAGGCGT GGAAGGGTGG GCAGTCACGC GAGAAGTGGC
AGCTCTAGGA GCCAAAATGG TGGTTCCGCA CCTTCCCACC CGTCAGTGCG CTCTTCACCG

      4030       4040       4050       4060       4070       4080
TGGCCGGCGG CAAGCCACAG GCCCCGGGTC GCCTCAACGA CCTGCGACAC ATCGTCTACA
ACCGGCCGCC GTTCGGTGTC CGGGGCCCAG CGGAGTTGCT GGACGCTGTG TAGCAGATGT

      4090       4100       4110       4120       4130       4140
AGTCTGCCGA CGCTCCGTGG CGCCGGGCAC GACGCAATCT CGGCCTGATG ATGCGGGAAG
TCAGACGGCT GCGAGGCACC GCGGCCCGTG CTGCGTTAGA GCCGGACTAC TACGCCCTTC

      4150       4160       4170       4180       4190       4200
GCCTGCTCAA GGAAAACATC GACGGCGAGG CGTTGATTTG GGCGCATGAG CGGCTGATGG
CGGACGAGTT CCTTTTGTAG CTGCCGCTCC GCAACTAAAC CCGCGTACTC GCCGACTACC
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FIG. 32G

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      4210       4220       4230       4240       4250       4260
CGCGGCGCGA ACAGCGGCGC ATCCTGATGA TGATTTCGGA CGGCGCGCCG GTCGACGACT
GCGCCGCGCT TGTCGCCGCG TAGGACTACT ACTAAAGCCT GCCGCGCGGC CAGCTGCTGA

      4270       4280       4290       4300       4310       4320
CGACGCTGTC GGTCAATCCA GGAAACTATC TGGAGCGTCA CCTGCGCGCG GTCATCGAGC
GCTGCGACAG CCAGTTAGGT CCTTTGATAG ACCTCGCAGT GGACGCGCGC CAGTAGCTCG

      4330       4340       4350       4360       4370       4380
AGATCGAAAC GCGCTCGCCG GTGGAACTGC TGGCGATCGG TATCGGCCAC GACGTGACGC
TCTAGCTTTG CGCGAGCGGC CACCTTGACG ACCGCTAGCC ATAGCCGGTG CTGCACTGCG

      4390       4400       4410       4420       4430       4440
GCTACTATCG CCGTGCCGTC ACCATCGTCG ATGCCGATGA GCTTGCCGGC GCGATGACCG
CGATGATAGC GGCACGGCAG TGGTAGCAGC TACGGCTACT CGAACGGCCG CGCTACTGGC

      4450       4460       4470       4480       4490       4500
AACAGCTGGC CGCACTCTTC GAGGACGAAA GCCAGCGCCG CGGTTCTTCG CGTCTTCGCC
TTGTCGACCG GCGTGAGAAG CTCCTGCTTT CGGTCGCGGC GCCAAGAAGC GCAGAAGCGG

      4510       4520       4530       4540       4550       4560
GCGCCGGGTG ATGCTTCCCC CTTGGGGGCG GTGGAACATC GCCTCCGAGC TGCCAATCGG
CGCGGCCCAC TACGAAGGGG GAACCCCCGC CACCTTGTAG CGGAGGCTCG ACGGTTAGCC

      4570       4580       4590       4600       4610       4620
CACCTGCACG CATCGCTGGC GGCCGAAGTC AATTTACGGA CATAGTTTTA CAGTCTACCA
GTGGACGTGC GTAGCGACCG CCGGCTTCAG TTAAATGCCT GTATCAAAAT GTCAGATGGT

      4630       4640       4650       4660       4670       4680
AGCTACCATG CGTGGCGGGC TCACTTTGAG CGCACGCCGC GTCATTCCCG ATGCCCCCTG
TCGATGGTAC GCACCGCCCG AGTGAAACTC GCGTGCGGCG CAGTAAGGGC TACGGGGGAC

      4690       4700       4710       4720       4730       4740
AAGGTACTTC TCTTGATGCT TGGCCGCGGT CTCCTAGCCC TTTTCCTCCT GGCTTCGGCC
TTCCATGAAG AGAACTACGA ACCGGCGCCA GAGGATCGGG AAAAGGAGGA CCGAAGCCGG

      4750       4760       4770       4780       4790       4800
TGCCCGGC
ACGGGCCG
```

FIG. 32H

```
        10         20         30         40         50         60
GAGCTCATAG AGCAGTTCCT CGATCGACTT CAGCAGTCGC ATGAAATCCA TGCCGTGCTC
CTCGAGTATC TCGTCAAGGA GCTAGCTGAA GTCGTCAGCG TACTTTAGGT ACGGCACGAG

        70         80         90        100        110        120
CCCTTGCTTC TATGCGTGGC ACGACCGCGC GCCGGGGCCG ATGCCGGTCA GTCGCGCAGA
GGGAACGAAG ATACGCACCG TGCTGGCGCG CGGCCCCGGC TACGGCCAGT CAGCGCGTCT

       130        140        150        160        170        180
CGCAGCTCGT CGGTACGCAT CTGCAGCATC TCCAGCGTCG ACAGGAAGCT CATGCCGAGC
GCGTCGAGCA GCCATGCGTA GACGTCGTAG AGGTCGCAGC TGTCCTTCGA GTACGGCTCG

       190        200        210        220        230        240
AGGCTCTGAT CGAGCTTGCC CTTGGCTGCG ACCGTTGCGC CGATGTTGCG GCGGGTGATC
TCCGAGACTA GCTCGAACGG GAACCGACGC TGGCAACGCG GCTACAACGC CGCCCACTAG

       250        260        270        280        290        300
GGGCCGATCG AGATCTCCTG AAGCATCACG GGGGCTGCCT GGGCCCGGCC ATTGGCTGTC
CCCGGCTAGC TCTAGAGGAC TTCGTAGTGC CCCCGACGGA CCCGGGCCGG TAACCGACAG

       310        320        330        340        350        360
ATGACCGTGA CGATAAAGTT GAGGTTGGCC GGGTCGAGGC CGATCTTTTC CGCATCTTCA
TACTGGCACT GCTATTTCAA CTCCAACCGG CCCAGCTCCG GCTAGAAAAG GCGTAGAAGT

       370        380        390        400        410        420
TAGGTGAGCG CGATGTTGCT GGCGCCGGTA TCGACCAGCA TGCTGATGTC CTTGCCGTCG
ATCCACTCGC GCTACAACGA CCGCGGCCAT AGCTGGTCGT ACGACTACAG GAACGGCAGC

       430        440        450        460        470        480
ACCGTCGCAG TGGTCTCGAA ATGACCGTTC AGCATCTTCT GCAGCACCAC TTCCTGCTGT
TGGCAGCGTC ACCAGAGCTT TACTGGCAAG TCGTAGAAGA CGTCGTGGTG AAGGACGACA

       490        500        510        520        530        540
CCCTCGCTGT CAGTGATGAT GGTGGCGCGG CCGGGGATGA GGCCGGCGAG CAGGCGGTTA
GGGAGCGACA GTCACTACTA CCACCGCGCC GGCCCCTACT CCGGCCGCTC GTCCGCCAAT

       550        560        570        580        590        600
CCGAAGCCCT CCAACTCGAA GCGGTAGACA TAGGCCGAGA CCAGCGCCAG AACGACGAAG
GGCTTCGGGA GGTTGAGCTT CGCCATCTGT ATCCGGCTCT GGTCGCGGTC TTGCTGCTTC
```

FIG. 33A

```
       610        620        630        640        650        660
AGCCAGATGG CGATCTGACG CAGGCCTTCG CCGAAGCGGT GGCGGCTCTG CAGGATGCCG
TCGGTCTACC GCTAGACTGC GTCCGGAAGC GGCTTCGCCA CCGCCGAGAC GTCCTACGGC

       670        680        690        700        710        720
GCGCCGATCA GCGTGGCGAT GGCGCCGAGC GAGACCAGTT GCCCGAACTG GTCATTGGCA
CGCGGCTAGT CGCACCGCTA CCGCGGCTCG CTCTGGTCAA CGGGCTTGAC CAGTAACCGT

       730        740        750        760        770        780
AGCCCCATGG TGCGGCCGGT GTCGTGGTTG ATGATCAGCA GGATGAGGCC GATGGCCAGG
TCGGGGTACC ACGCCGGCCA CAGCACCAAC TACTAGTCGT CCTACTCCGG CTACCGGTCC

       790        800        810        820        830        840
ATCGAGAGCA GGATGGCAAG ACGGGTCATG CTTCGCCGCG TTCCCTCGCC ATGCGCGTGC
TAGCTCTCGT CCTACCGTTC TGCCCAGTAC GAAGCGGCGC AAGGGAGCGG TACGCGCACG

       850        860        870        880        890        900
GTCGGGTTTC GCGCCGCGGC TTGCGTTCGA CGGTCTCAAG CCGTGCAGGC AACGCGCTCA
CAGCCCAAAG CGCGGCGCCG AACGCAAGCT GCCAGAGTTC GGCACGTCCG TTGCGCGAGT

       910        920        930        940        950        960
TGATCGCGCG GCGTTCGGCA TCGGTATAGA GCGTCCAGCG TCCGACTTCG TCGCGGGTAC
ACTAGCGCGC CGCAAGCCGT AGCCATATCT CGCAGGTCGC AGGCTGAAGC AGCGCCCATG

       970        980        990       1000       1010       1020
GGCCGCAGCC GAAACAGTAG CCGGTCTTGT CATCGATCGA ACAGACGAGA ATGCAGGGAG
CCGGCGTCGG CTTTGTCATC GGCCAGAACA GTAGCTAGCT TGTCTGCTCT TACGTCCCTC

      1030       1040       1050       1060       1070       1080
ATTCCATGGG CGTGCTCAGT TTTCCCTTGA TATATCGATG TTTCAAACCG TCAGCGCAAG
TAAGGTACCC GCACGAGTCA AAAGGGAACT ATATAGCTAC AAAGTTTGGC AGTCGCGTTC

      1090       1100       1110       1120       1130       1140
GGCACCGAGC ACGGCGATTT CGGTCAGTTG CTGCGTCGCC CCGATCGTGT CGCCCGTTTG
CCGTGGCTCG TGCCGCTAAA GCCAGTCAAC GACGCAGCGG GGCTAGCACA GCGGGCAAAC

      1150       1160       1170       1180       1190       1200
TCCGCCGATC TTGCGCATCG CCAGCCGAGC GAAGCCCTTG ACCGTGGCAA GGAATGCGAC
AGGCGGCTAG AACGCGTAGC GGTCGGCTCG CTTCGGGAAC TGGCACCGTT CCTTACGCTG
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FIG. 33B

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      1210       1220       1230       1240       1250       1260
GAGCGCCGCG ATGACGCCGA GCGCCGGGAC CTGCGCGAGA TAGAAGAGCA GCATTGCGAC
CTCGCGGCGC TACTGCGGCT CGCGGCCCTG GACGCGCTCT ATCTTCTCGT CGTAACGCTG

      1270       1280       1290       1300       1310       1320
AAGAAGTCCG AAGGCAAGCG CGAAGCGCGT GGCCGCCGGT TCCGGCTCGC CAGCCGAGGC
TTCTTCAGGC TTCCGTTCGC GCTTCGCGCA CCGGCGGCCA AGGCCGAGCG GTCGGCTCCG

      1330       1340       1350       1360       1370       1380
CGCGACGCCG CTGCTGCGCG CCGGCGGAAG CGACGACCAG TGCCAGACCA TGGCGGCGCG
GCGCTGCGGC GACGACGCGC GGCCGCCTTC GCTGCTGGTC ACGGTCTGGT ACCGCCGCGC

      1390       1400       1410       1420       1430       1440
GCTGAGGCAC GCTGCGCCAA GGATCGCCAT GGCGGCGCCC AGCGGCGAAA AGAGCGGCAG
CGACTCCGTG CGACGCGGTT CCTAGCGGTA CCGCCGCGGG TCGCCGCTTT TCTCGCCGTC

      1450       1460       1470       1480       1490       1500
GATCGAGGCG AACGCCGAGA CGCGCAGGCC GAAGGAGAGG ATGAGGGCGA CGGCCGCATA
CTAGCTCCGC TTGCGGCTCT GCGCGTCCGG CTTCCTCTCC TACTCCCGCT GCCGGCGTAT

      1510       1520       1530       1540       1550       1560
GGTGCCGATG CGGCTGTCCT TCATGATCGC AAGCGCCGCT TCGCGGTCGC GACCGCCGCC
CCACGGCTAC GCCGACAGGA AGTACTAGCG TTCGCGGCGA AGCGCCAGCG CTGGCGGCGG

      1570       1580       1590       1600       1610       1620
AAAGCCATCG GCCGTGTCGC CAAGCCCGTC TTCGTGCAGT GCGCCGGTGA CAAGCGCCTG
TTTCGGTAGC CGGCACAGCG GTTCGGGCAG AAGCACGTCA CGCGGCCACT GTTCGCGGAC

      1630       1640       1650       1660       1670       1680
GATGGCGACG ACGACAAAGG CGGCAAAGAG CGAGCTCACC TGCAGCGCCA TGAGGGCCAT
CTACCGCTGC TGCTGTTTCC GCCGTTTCTC GCTCGAGTGG ACGTCGCGGT ACTCCCGGTA

      1690       1700       1710       1720       1730       1740
GGCGACGGCC GCCGATGGCA GTGCGATCGC CAGGCCGGCG AACGGGAAGG CGCGCACGGC
CCGCTGCCGG CGGCTACCGT CACGCTAGCG GTCCGGCCGC TTGCCCTTCC GCGCGTGCCG

      1750       1760       1770       1780       1790       1800
ACGGCTCAAG CGCCCGTCAT AACCTTCGAA ATGACGCGCA GGCATCGGGA TGCGGCTGAG
TGCCGAGTTC GCGGGCAGTA TTGGAAGCTT TACTGCGCGT CCGTAGCCCT ACGCCGACTC
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FIG. 33C

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      1810       1820       1830       1840       1850       1860
AAAGCCGATC GACCGCGCCA CATCGTCACA GAAATCGCCA ACGAAGCCCA TGGCTCCTCC
TTTCGGCTAG CTGGCGCGGT GTAGCAGTGT CTTTAGCGGT TGCTTCGGGT ACCGAGGAGG

      1870       1880       1890       1900       1910       1920
AAGGTTGCGG CCATTGACCC GGCCGCTGCC AAACTCGCCG ACTGCGGCGA GTCTCGCAAG
TTCCAACGCC GGTAACTGGG CCGGCGACGG TTTGAGCGGC TGACGCCGCT CAGAGCGTTC

      1930       1940       1950       1960       1970       1980
CCGGGCGGGC GCACCCGCGA GGGCCGCGCA CACTTTTCCC AGACCTTTCA TAGGCCGTCT
GGCCCGCCCG CGTGGGCGCT CCCGGCGCGT GTGAAAAGGG TCTGGAAAGT ATCCGGCAGA

      1990       2000       2010       2020       2030       2040
GCGACCGCTC GCGGATCGAG ACGGCGACGC CGATTGGCGC AAATGTCGTT GCCCGAATTT
CGCTGGCGAG CGCCTAGCTC TGCCGCTGCG GCTAACCGCG TTTACAGCAA CGGGCTTAAA

      2050       2060       2070       2080       2090       2100
TCGGCGCCCT CTATGAGGGG CGTAGATAGA GCTTCACGAT GATGCAAGGA TTCCTCCCAT
AGCCGCGGGA GATACTCCCC GCATCTATCT CGAAGTGCTA CTACGTTCCT AAGGAGGGTA

      2110       2120       2130       2140       2150       2160
GAGTGCCAGC GGCCTGCCGT TTGATGATTT TCGCGAATTG TTGCGCAACC TGCCGGGCCC
CTCACGGTCG CCGGACGGCA AACTACTAAA AGCGCTTAAC AACGCGTTGG ACGGCCCGGG

      2170       2180       2190       2200       2210       2220
GGATGCGGCA GCCCTCGTTG CCGCGCGGGA GCGGGACGCC CAGCTGACGA AGCCGCCGGG
CCTACGCCGT CGGGAGCAAC GGCGCGCCCT CGCCCTGCGG GTCGACTGCT TCGGCGGCCC

      2230       2240       2250       2260       2270       2280
CGCGCTCGGC CGCCTCGAGG AAATCGCCTT CTGGCTCGCC GCCTGGACGG GCAAGGCGCC
GCGCGAGCCG GCGGAGCTCC TTTAGCGGAA GACCGAGCGG CGGACCTGCC CGTTCCGCGG

      2290       2300       2310       2320       2330       2340
GGTGGTCAAC CGGCCGCTGG TGGCGATCTT TGCCGGCAAC CACGGCGTCA CCCGCCAGGG
CCACCAGTTG GCCGGCGACC ACCGCTAGAA ACGGCCGTTG GTGCCGCAGT GGGCGGTCCC

      2350       2360       2370       2380       2390       2400
GGTGACCCCG TTCCCGTCAT CCGTCACCGC ACAGATGGTC GAGAATTTTG CCGCCGGTGG
CCACTGGGGC AAGGGCAGTA GGCAGTGGCG TGTCTACCAG CTCTTAAAAC GGCGGCCACC
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FIG. 33D

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      2410       2420       2430       2440       2450       2460
CGCTGCGATC AACCAGATCT GCGTCAGCCA CGACCTCGGG CTGAAGGTCT TCGACCTCGC
GCGACGCTAG TTGGTCTAGA CGCAGTCGGT GCTGGAGCCC GACTTCCAGA AGCTGGAGCG

      2470       2480       2490       2500       2510       2520
ACTCGAATAC CCGACCGGTG ATATCACCGA GGAAGCCGCG CTGTCCGAGC GCGATTGCGC
TGAGCTTATG GGCTGGCCAC TATAGTGGCT CCTTCGGCGC GACAGGCTCG CGCTAACGCG

      2530       2540       2550       2560       2570       2580
CGCGACCATG GCCTTTGGCA TGGAGGCGAT TGCCGGCGGC ACGGATCTTC TGTGCATCGG
GCGCTGGTAC CGGAAACCGT ACCTCCGCTA ACGGCCGCCG TGCCTAGAAG ACACGTAGCC

      2590       2600       2610       2620       2630       2640
CGAAATGGGC ATCGGCAACA CCACGATCGC GGCCGCGATC AATCTCGGCC TTTATGGTGG
GCTTTACCCG TAGCCGTTGT GGTGCTAGCG CCGGCGCTAG TTAGAGCCGG AAATACCACC

      2650       2660       2670       2680       2690       2700
CACGGCCGAA GAATGGGTCG GTCCGGGTAC CGGCTCCGAG GGCGAGGTGC TGAAGCGCAA
GTGCCGGCTT CTTACCCAGC CAGGCCCATG GCCGAGGCTC CCGCTCCACG ACTTCGCGTT

      2710       2720       2730       2740       2750       2760
GATCGCCGCG GTCGAAAAGG CCGTGGCGCT GCATCGCGAT CACCTGTCCG ATCCGCTCGA
CTAGCGGCGC CAGCTTTTCC GGCACCGCGA CGTAGCGCTA GTGGACAGGC TAGGCGAGCT

      2770       2780       2790       2800       2810       2820
ACTGATGCGT CGCCTCGGCG GTCGTGAGAT CGCGGCCATG GCTGGCGCCA TCCTGGCCGC
TGACTACGCA GCGGAGCCGC CAGCACTCTA GCGCCGGTAC CGACCGCGGT AGGACCGGCG

      2830       2840       2850       2860       2870       2880
CCGCGTCCAG AAGGTACCTG TCATCATCGA CGGCTACGTG GCGACCGCTG CGGCTTCGAT
GGCGCAGGTC TTCCATGGAC AGTAGTAGCT GCCGATGCAC CGCTGGCGAC GCCGAAGCTA

      2890       2900       2910       2920       2930       2940
CCTGAAGGCG GCCAACCCGT CGGCCCTCGA CCATTGCCTG ATCGGCCATG TTTCGGGCGA
GGACTTCCGC CGGTTGGGCA GCCGGGAGCT GGTAACGGAC TAGCCGGTAC AAAGCCCGCT

      2950       2960       2970       2980       2990       3000
ACCGGGGCAT CTGCGCGCGA TCGAGAAGCT CGGCAAGACG CCGCTGCTGG CACTCGGCAT
TGGCCCCGTA GACGCGCGCT AGCTCTTCGA GCCGTTCTGC GGCGACGACC GTGAGCCGTA
```

FIG. 33E

```
      3010       3020       3030       3040       3050       3060
GCGGCTTGGC GAAGGCACGG GCGCGGCCCT TGCCGCCGGT ATCGTCAAGG CGGCGGCCGC
CGCCGAACCG CTTCCGTGCC CGCGCCGGGA ACGGCGGCCA TAGCAGTTCC GCCGCCGGCG

      3070       3080       3090       3100       3110       3120
TTGCCACAGC GGCATGGCGA CCTTTGCCCA GGCCGGCGTC AGCAACAAGG AATAGTGAAG
AACGGTGTCG CCGTACCGCT GGAAACGGGT CCGGCCGCAG TCGTTGTTCC TTATCACTTC

      3130       3140       3150       3160       3170       3180
TTCCGGCCGG GCTTTGCAGG AAGGCCGGCC GGTTTCTGTC CAAGGCCTGT CACGGGCGCG
AAGGCCGGCC CGAAACGTCC TTCCGGCCGG CCAAAGACAG GTTCCGGACA GTGCCCGCGC

      3190       3200       3210       3220       3230       3240
AAGCTGTCGC GTGCCGGGCC TTGATGGATG CGTCCTTCTC GCCTATCCAA AGCGCAAATG
TTCGACAGCG CACGGCCCGG AACTACCTAC GCAGGAAGAG CGGATAGGTT TCGCGTTTAC

      3250       3260       3270       3280       3290       3300
CGCGCCCTAG CTATAGTCTT GGGTGCCTGC AACCGAGACC GCCTTGCATT CGCCTCAATC
GCGCGGGATC GATATCAGAA CCCACGGACG TTGGCTCTGG CGGAACGTAA GCGGAGTTAG

      3310       3320       3330       3340       3350       3360
ACGATGTCGA AGCAAGCACA GTTTCAAGCC CTGTCGAGAC GAAATGGACG CCAAGAACAC
TGCTACAGCT TCGTTCGTGT CAAAGTTCGG GACAGCTCTG CTTTACCTGC GGTTCTTGTG

      3370       3380       3390       3400       3410       3420
CACGCACCGC ATTGGACAGA CGGGTCCTGT CGAGAAGCAG ACCGGCATTC GGCATCTCTT
GTGCGTGGCG TAACCTGTCT GCCCAGGACA GCTCTTCGTC TGGCCGTAAG CCGTAGAGAA

      3430       3440       3450       3460       3470       3480
TGCCGCTGCG AGCTATTCGC TCGGCGGCGC CAAGCGGCTG ATCGGCGAGG CTGCCTTTCG
ACGGCGACGC TCGATAAGCG AGCCGCCGCG GTTCGCCGAC TAGCCGCTCC GACGGAAAGC

      3490       3500       3510       3520       3530       3540
CCACGAGCTG ATCGCCTTTG CCGCCGCGAT GATCGCTTTC ATCATCGTCG GCGCAACCTT
GGTGCTCGAC TAGCGGAAAC GGCGGCGCTA CTAGCGAAAG TAGTAGCAGC CGCGTTGGAA

      3550       3560       3570       3580       3590       3600
CTTCCAATAT GTGGCGATGG CGATCCTGTT CCTGCTGATG ATGGCCTTCG AGGCGATCAA
GAAGGTTATA CACCGCTACC GCTAGGACAA GGACGACTAC TACCGGAAGC TCCGCTAGTT
```

FIG. 33F

```
      3610       3620       3630       3640       3650       3660
CACGGCAATC GAGGAAATTG TCGATCGCGT TTCTCCCGAA ATCTCGGAAA TGGGTAAGAA
GTGCCGTTAG CTCCTTTAAC AGCTAGCGCA AAGAGGGCTT TAGAGCCTTT ACCCATTCTT

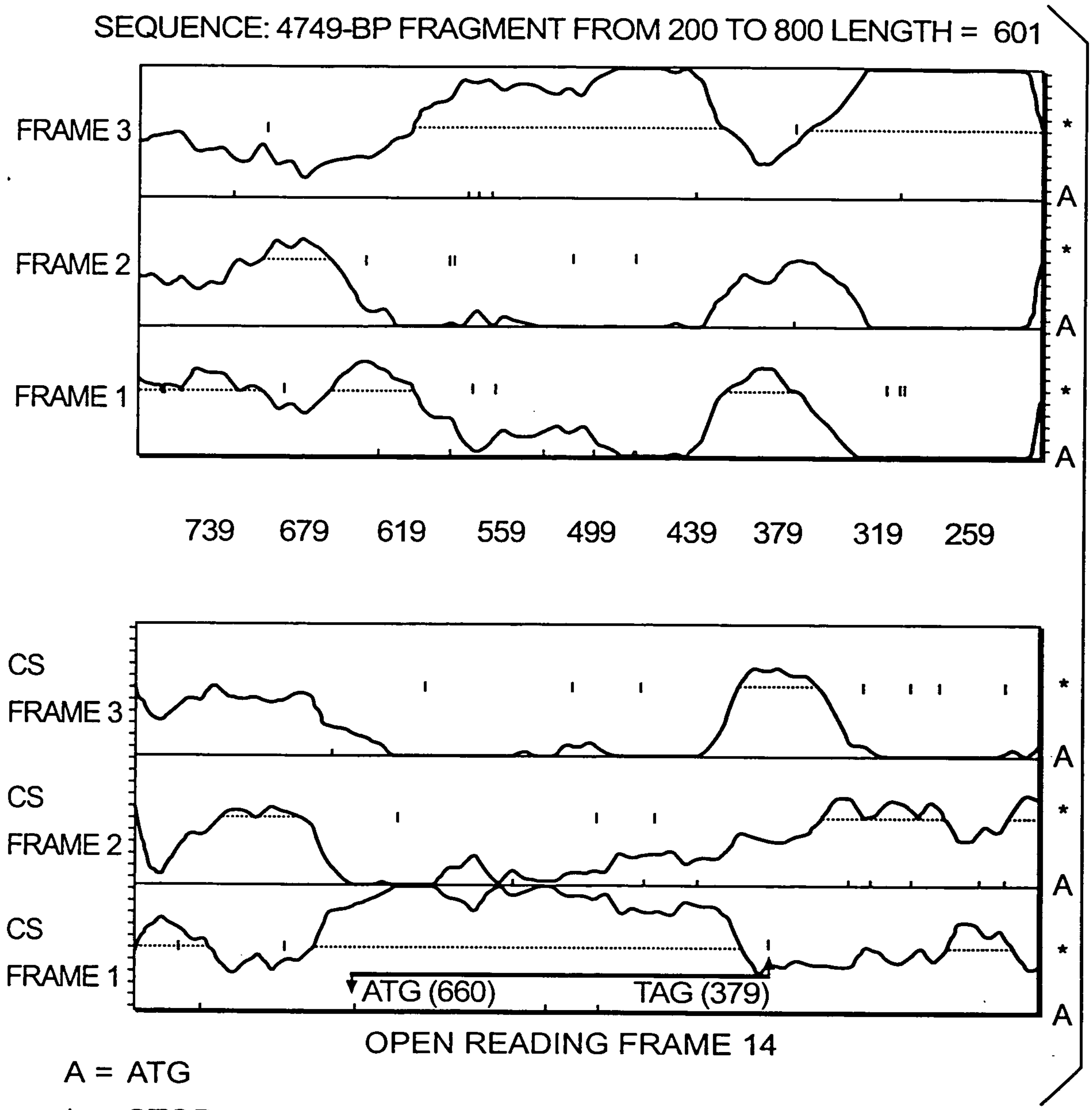
      3670       3680       3690       3700       3710       3720
CGCCAAGGAT CTCGGCTCCT TCGCCTGCCT CTGCCTGATT GTCGCCAACG GTGTCTATGC
GCGGTTCCTA GAGCCGAGGA AGCGGACGGA GACGGACTAA CAGCGGTTGC CACAGATACG

      3730       3740       3750       3760       3770       3780
CGCCTATGTC GTGATCTTCG ACGGCTTCAT GAACTGACCG GCTAGCGGGC CGGCGCCTTC
GCGGATACAG CACTAGAAGC TGCCGAAGTA CTTGACTGGC CGATCGCCCG GCCGCGGAAG

      3790       3800       3810       3820       3830       3840
ACCCGATAAA GCACATGCGG ACGCAGCGGG TTGCCCCCGG GTACCGTGAC GTCGTCGAAA
TGGGCTATTT CGTGTACGCC TGCGTCGCCC AACGGGGGCC CATGGCACTG CAGCAGCTTT

      3850       3860       3870       3880       3890       3900
TCATCAGCCG GATCC
AGTAGTCGGC CTAGG
```

FIG. 33G

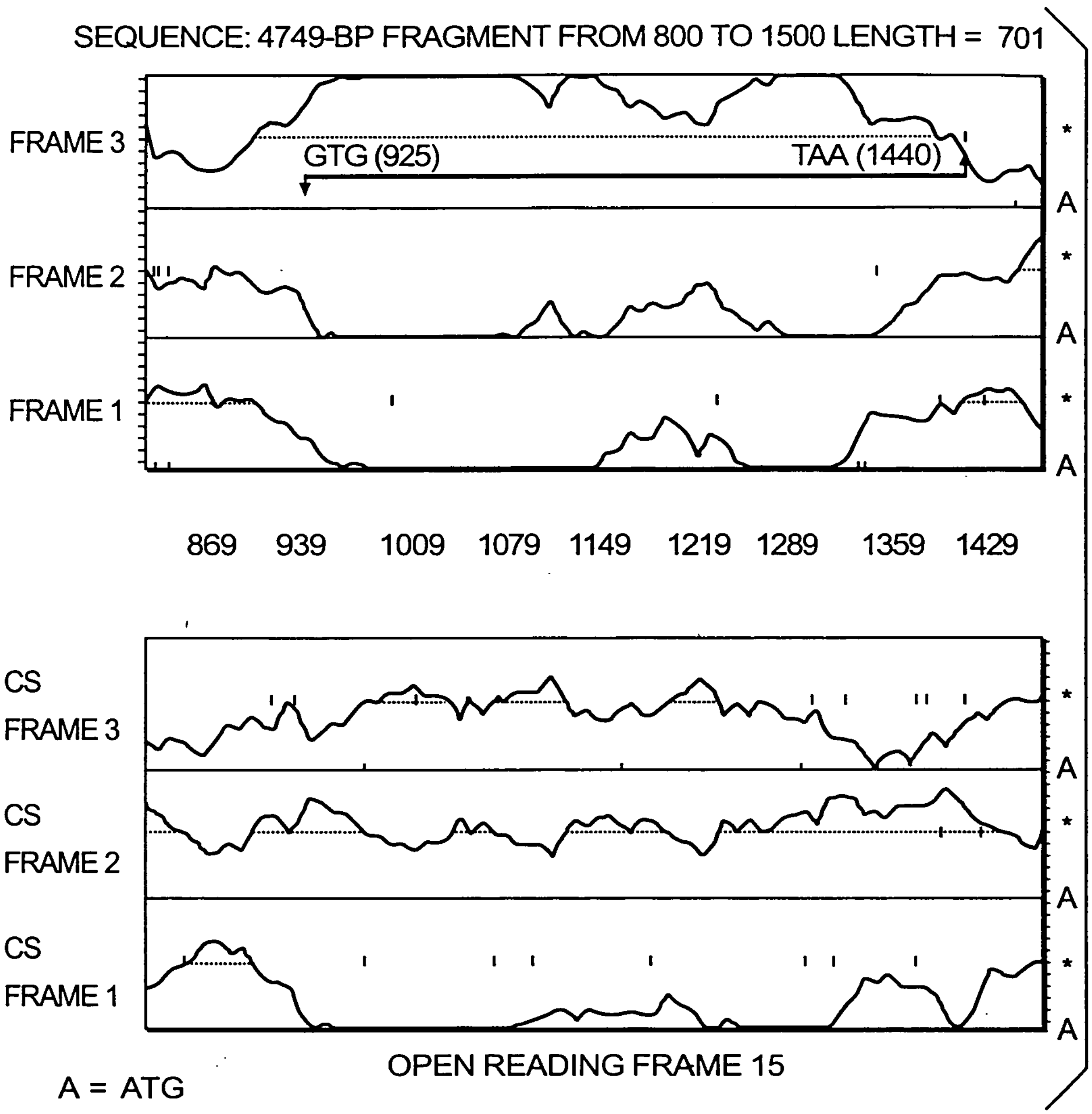


A = ATG

*: STOP

CS: COMPLEMENTARY STRAND

FIG. 34A

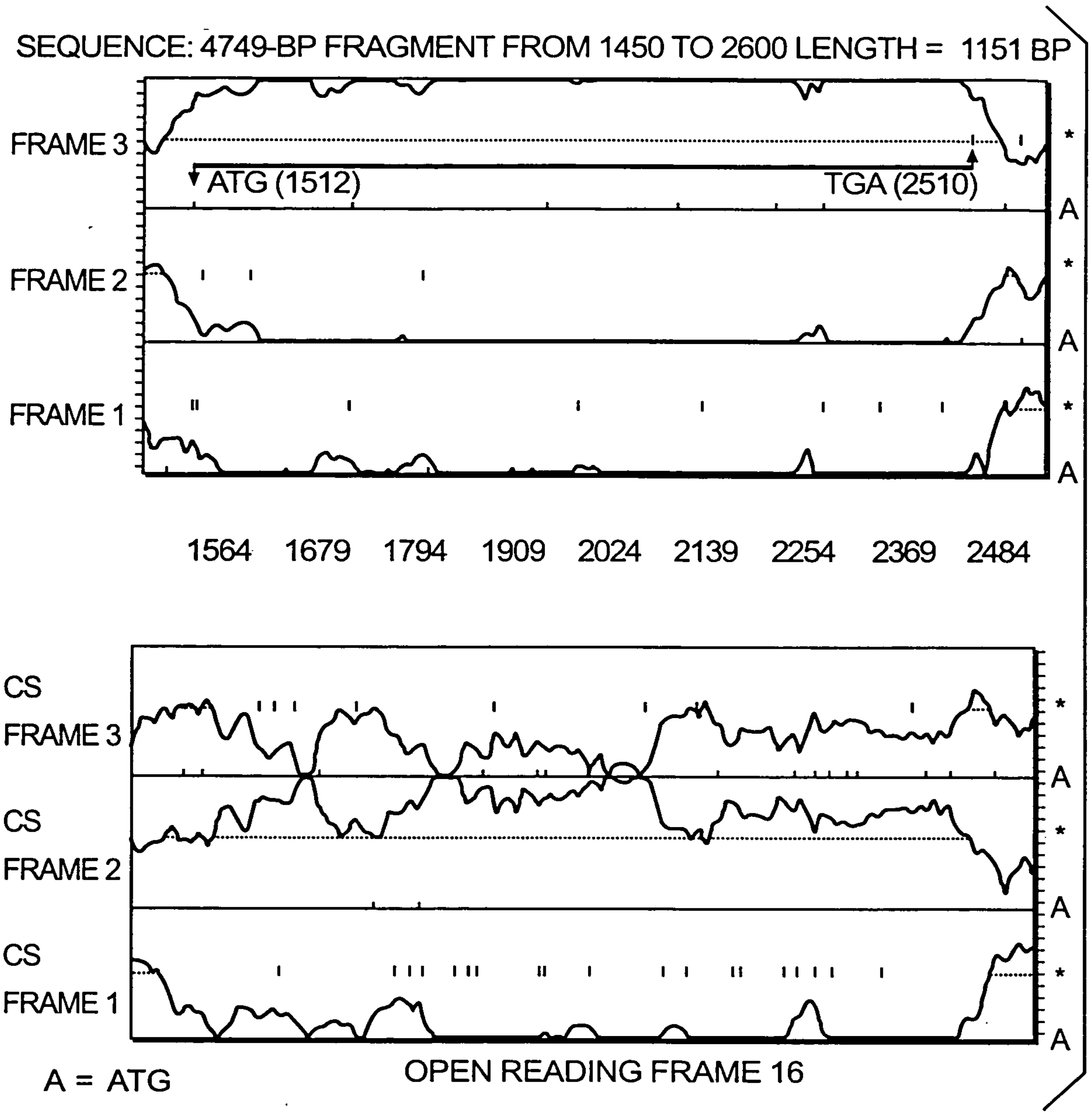


A = ATG

*: STOP

CS: COMPLEMENTARY STRAND

FIG. 34B

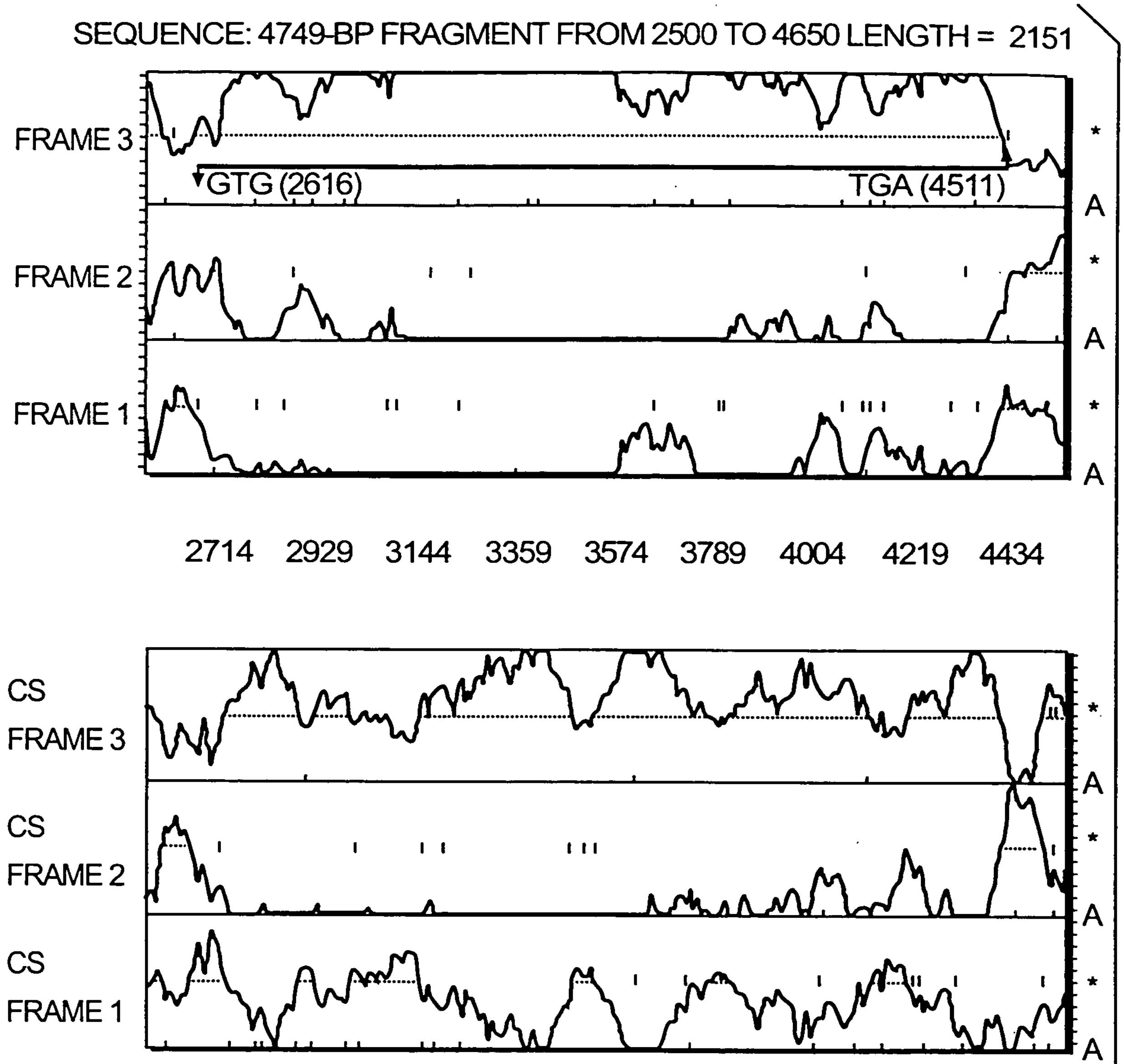


A = ATG

*: STOP

CS: COMPLEMENTARY STRAND

FIG. 34C



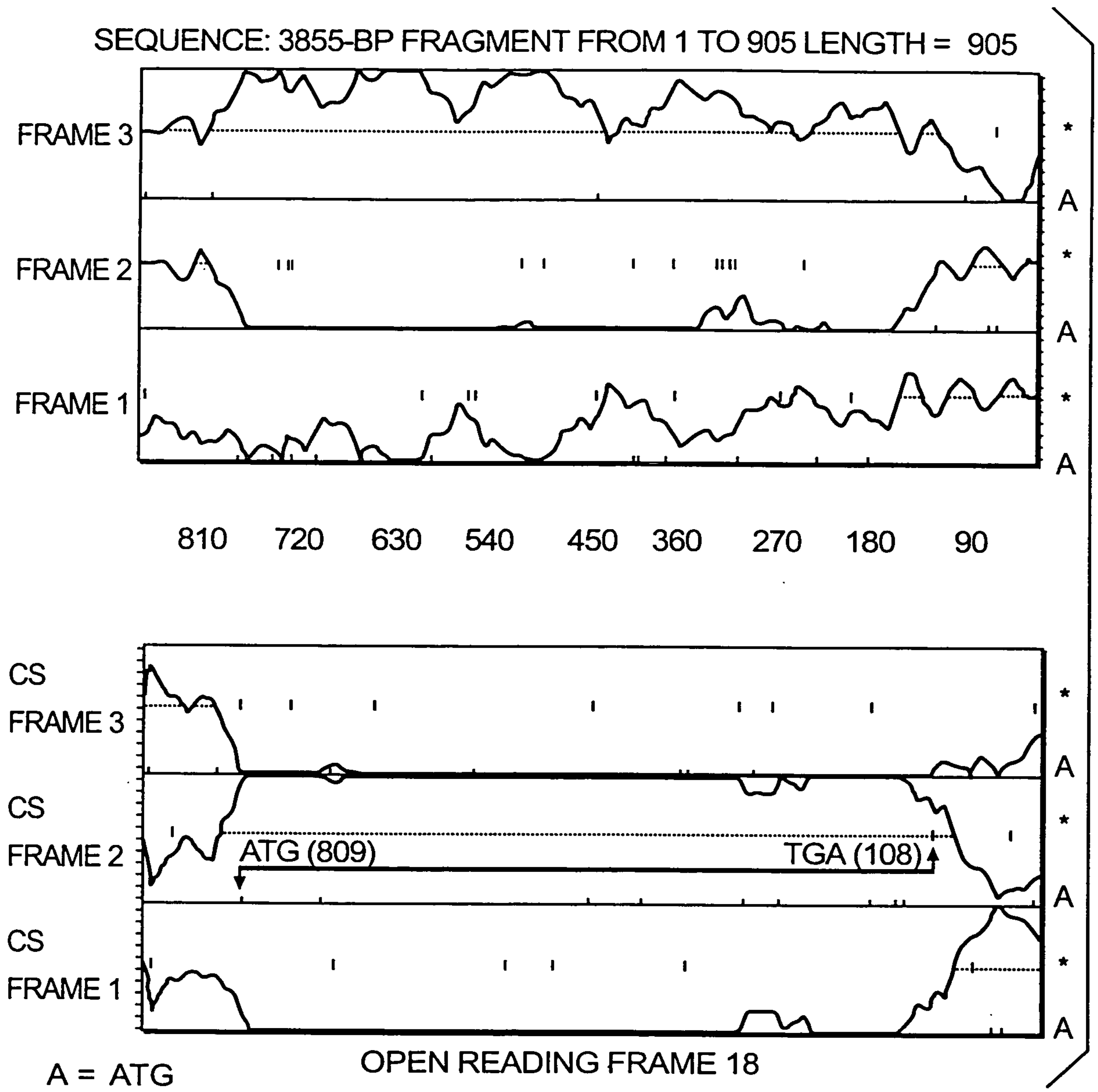
A = ATG

*: STOP

CS: COMPLEMENTARY STRAND

OPEN READING FRAME 17

FIG. 34D



A = ATG
*: STOP
CS: COMPLEMENTARY STRAND

FIG. 35A

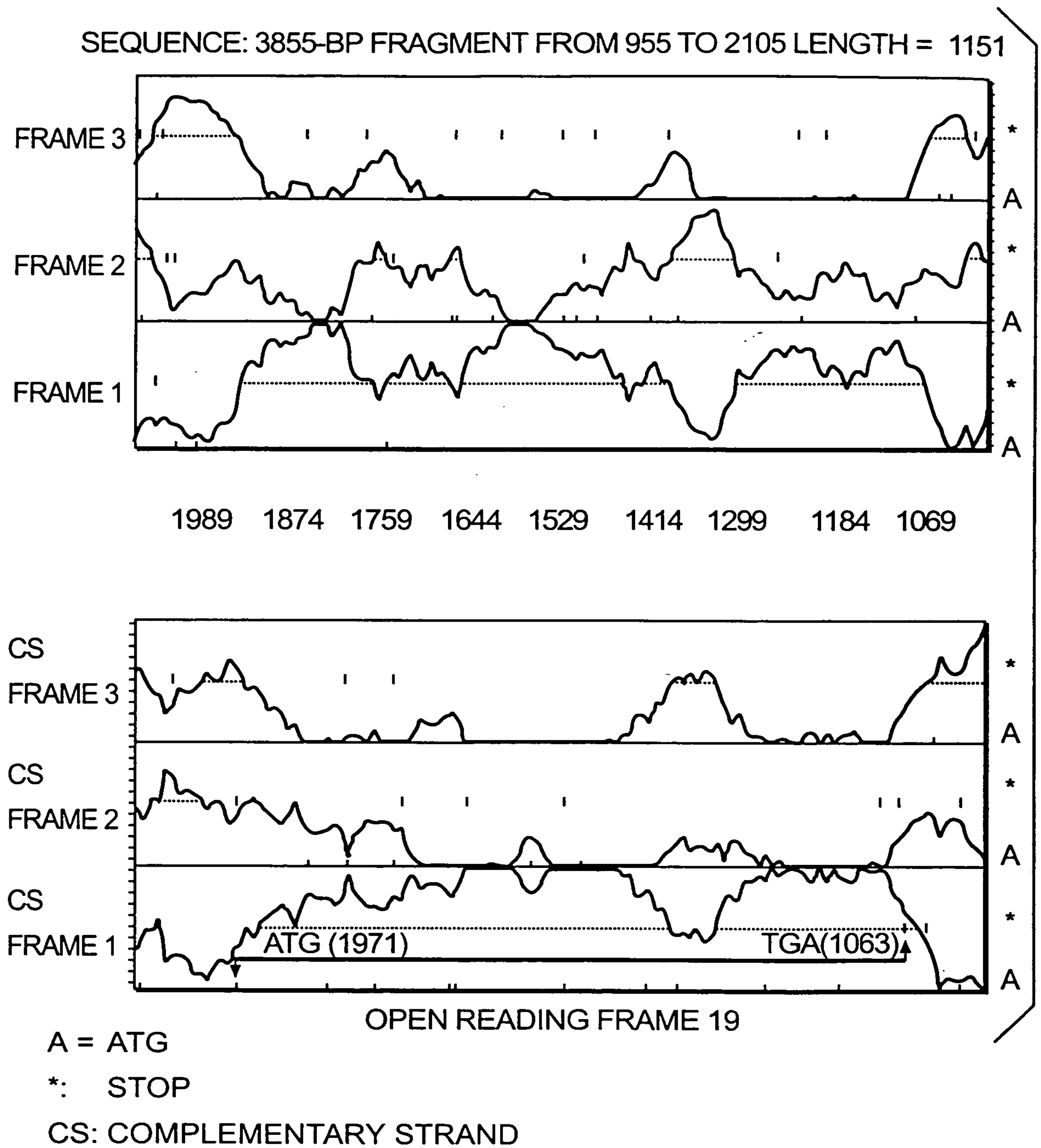
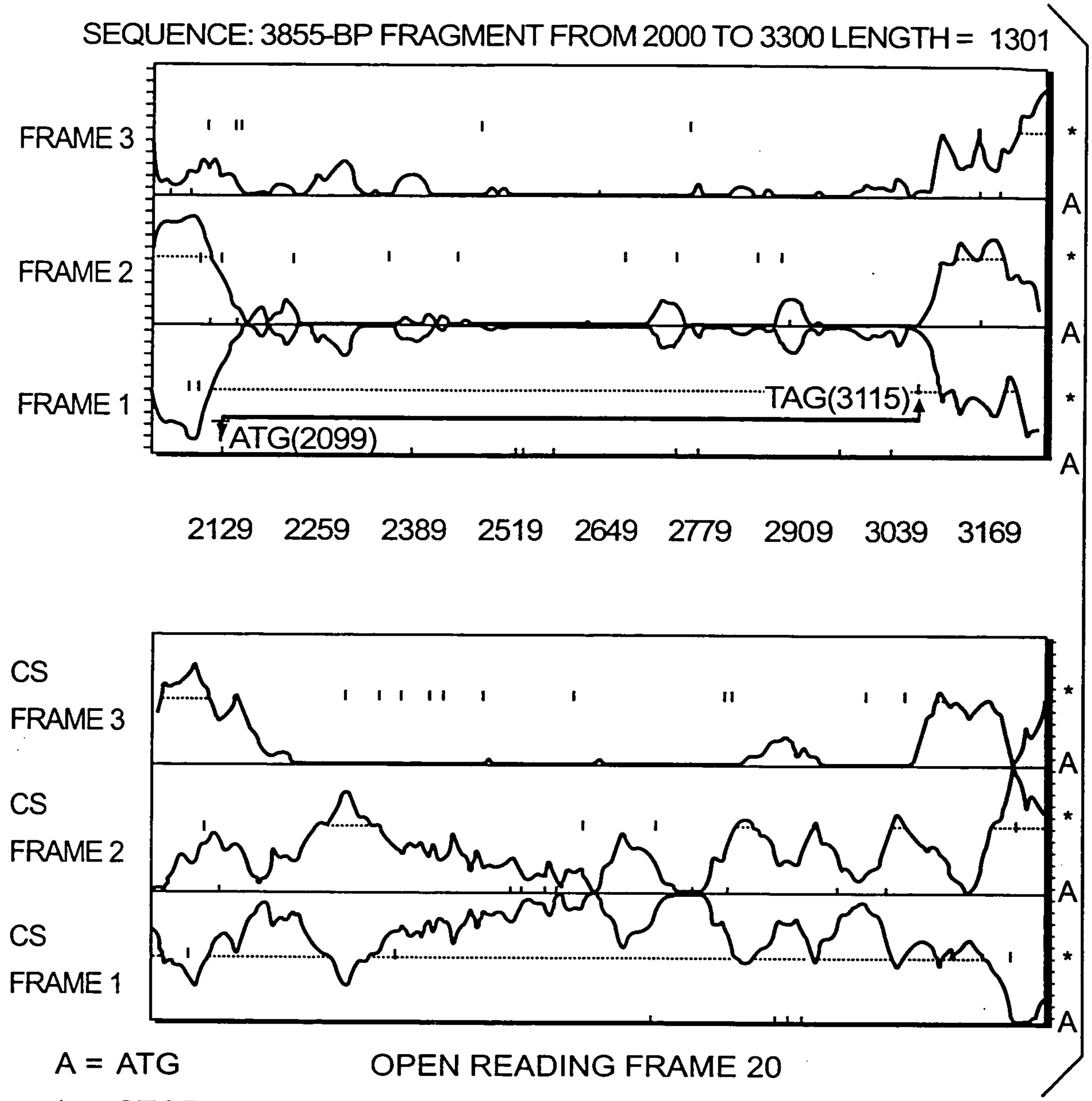

SEQUENCE: 3855-BP FRAGMENT FROM 955 TO 2105 LENGTH = 1151
FRAME 3
FRAME 2
FRAME 1
A
*
1989 1874 1759 1644 1529 1414 1299 1184 1069
CS FRAME 3
CS FRAME 2
CS FRAME 1
ATG (1971)
TGA(1063)
OPEN READING FRAME 19
A = ATG
*: STOP
CS: COMPLEMENTARY STRAND

FIG. 35B



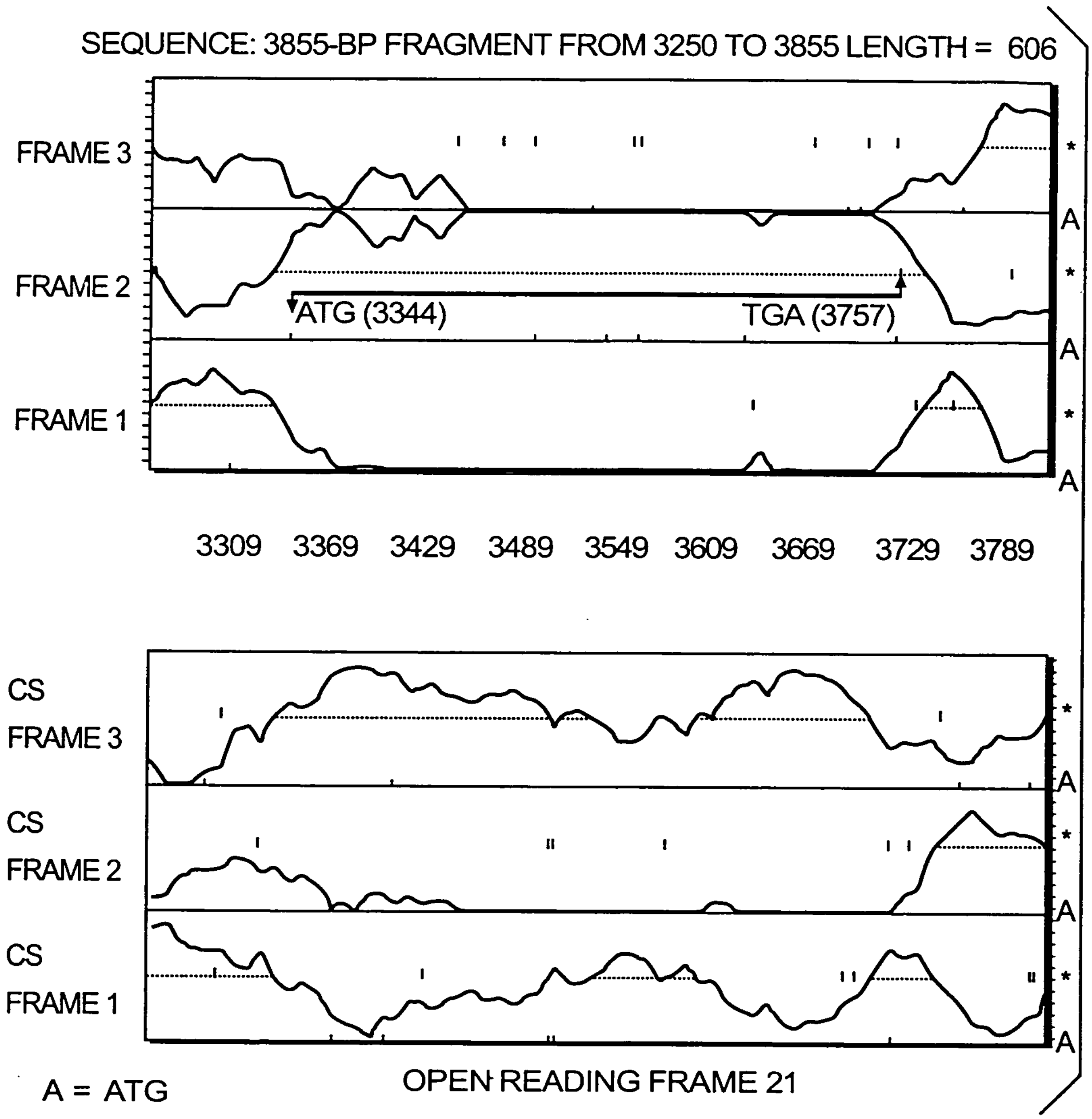
A = ATG

*: STOP

CS: COMPLEMENTARY STRAND

OPEN READING FRAME 20

FIG. 35C



A = ATG

*: STOP

CS: COMPLEMENTARY STRAND

FIG. 35D

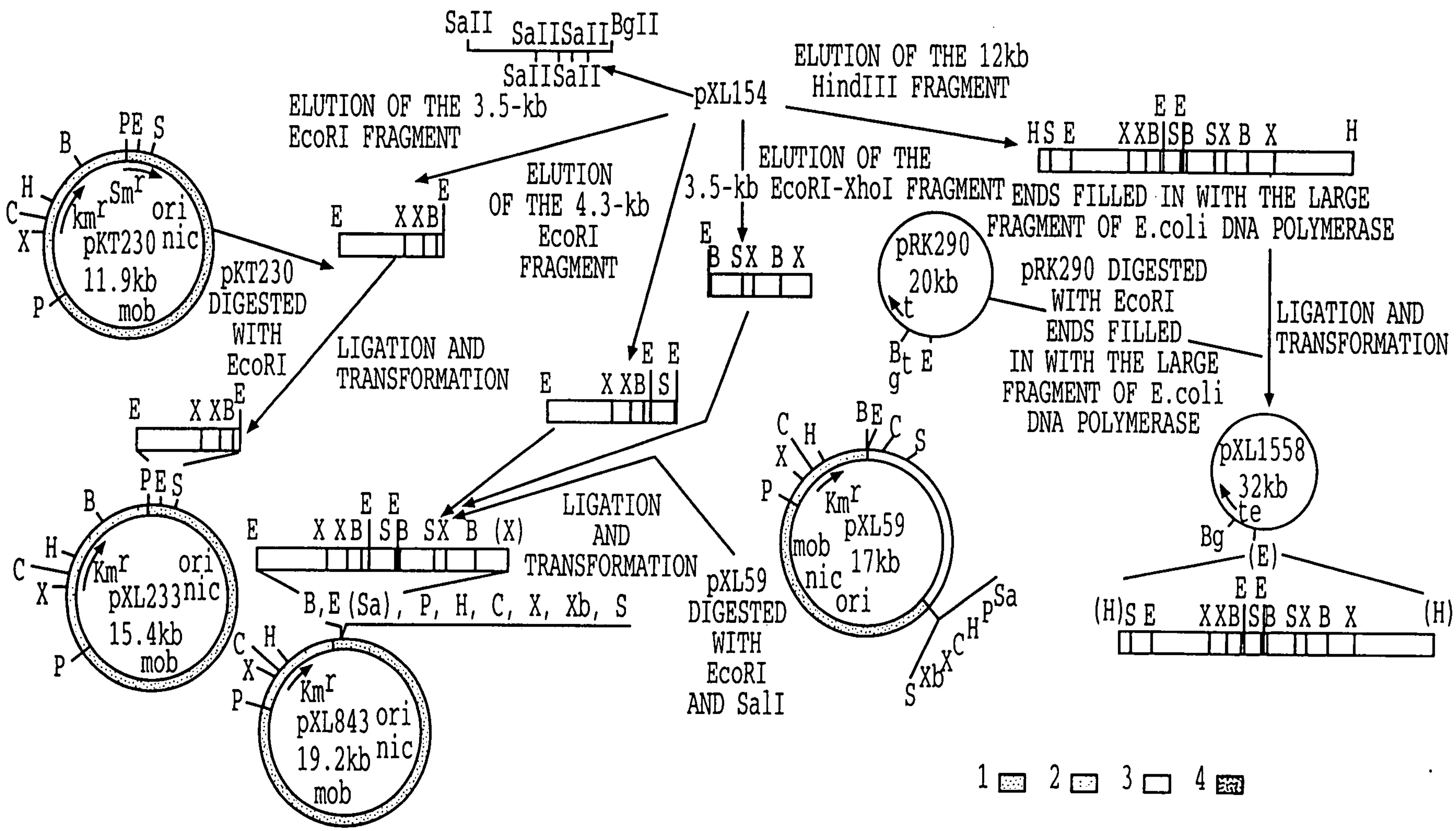

SalI SalISalI BglI SalISalI
pXL154
ELUTION OF THE 12kb HindIII FRAGMENT
ELUTION OF THE 3.5-kb EcoRI FRAGMENT
ELUTION OF THE 4.3-kb EcoRI FRAGMENT
ELUTION OF THE 3.5-kb EcoRI-XhoI FRAGMENT
ENDS FILLED IN WITH THE LARGE FRAGMENT OF E.coli DNA POLYMERASE
pKT230 11.9kb
pKT230 DIGESTED WITH EcoRI
LIGATION AND TRANSFORMATION
pXL233 15.4kb
LIGATION AND TRANSFORMATION
B,E (Sa), P, H, C, X, Xb, S
pXL843 19.2kb
pXL59 DIGESTED WITH EcoRI AND SalI
pXL59 17kb
pRK290 20kb
pRK290 DIGESTED WITH EcoRI ENDS FILLED IN WITH THE LARGE FRAGMENT OF E.coli DNA POLYMERASE
LIGATION AND TRANSFORMATION
pXL1558 32kb
1 2 3 4

FIG. 36

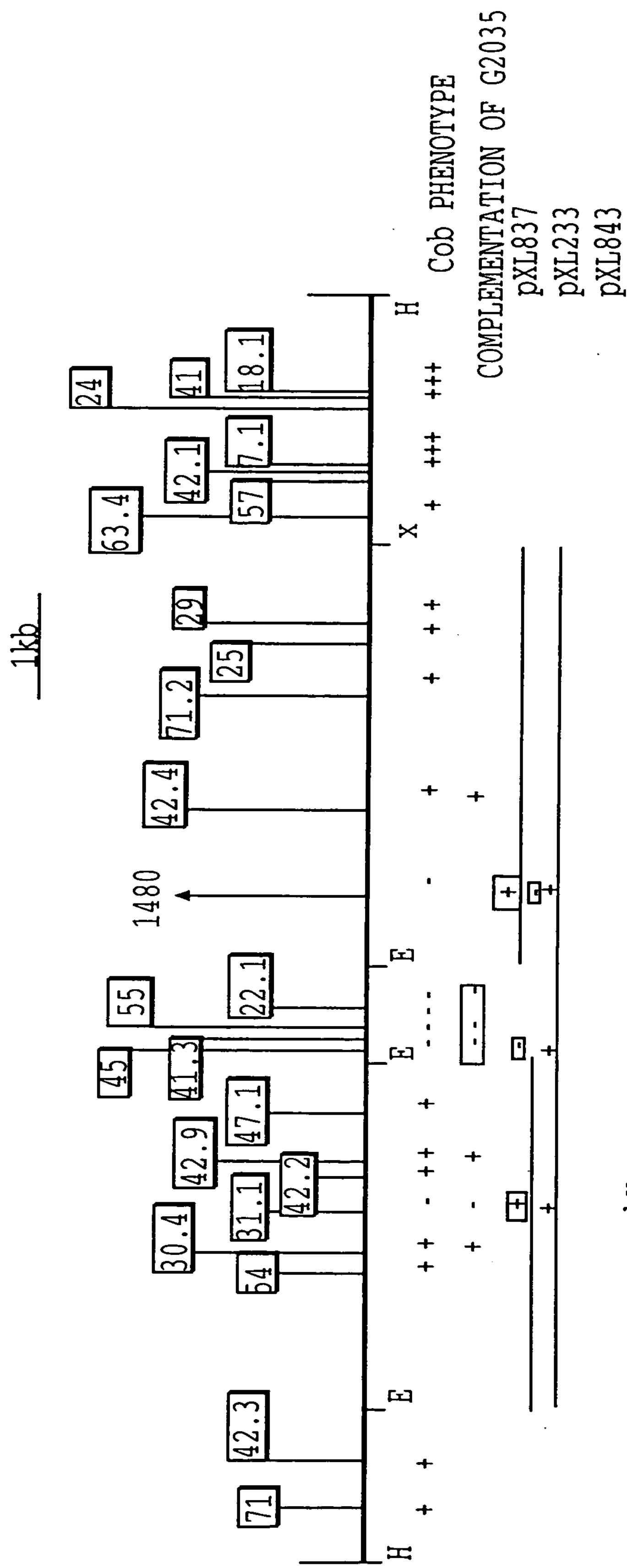

1kb
Cob PHENOTYPE
COMPLEMENTATION OF G2035
pXL837
pXL233
pXL843
H
E
E
E
X
H
1480
71
42.3
30.4
54
31.1
42.2
42.9
47.1
45
41.3
55
22.1
42.4
71.2
25
29
63.4
57
42.1
7.1
24
41
18.1
cobX
ORF 14
ORF 15
cobS
ORF 16
cobT
ORF 17

FIG. 37

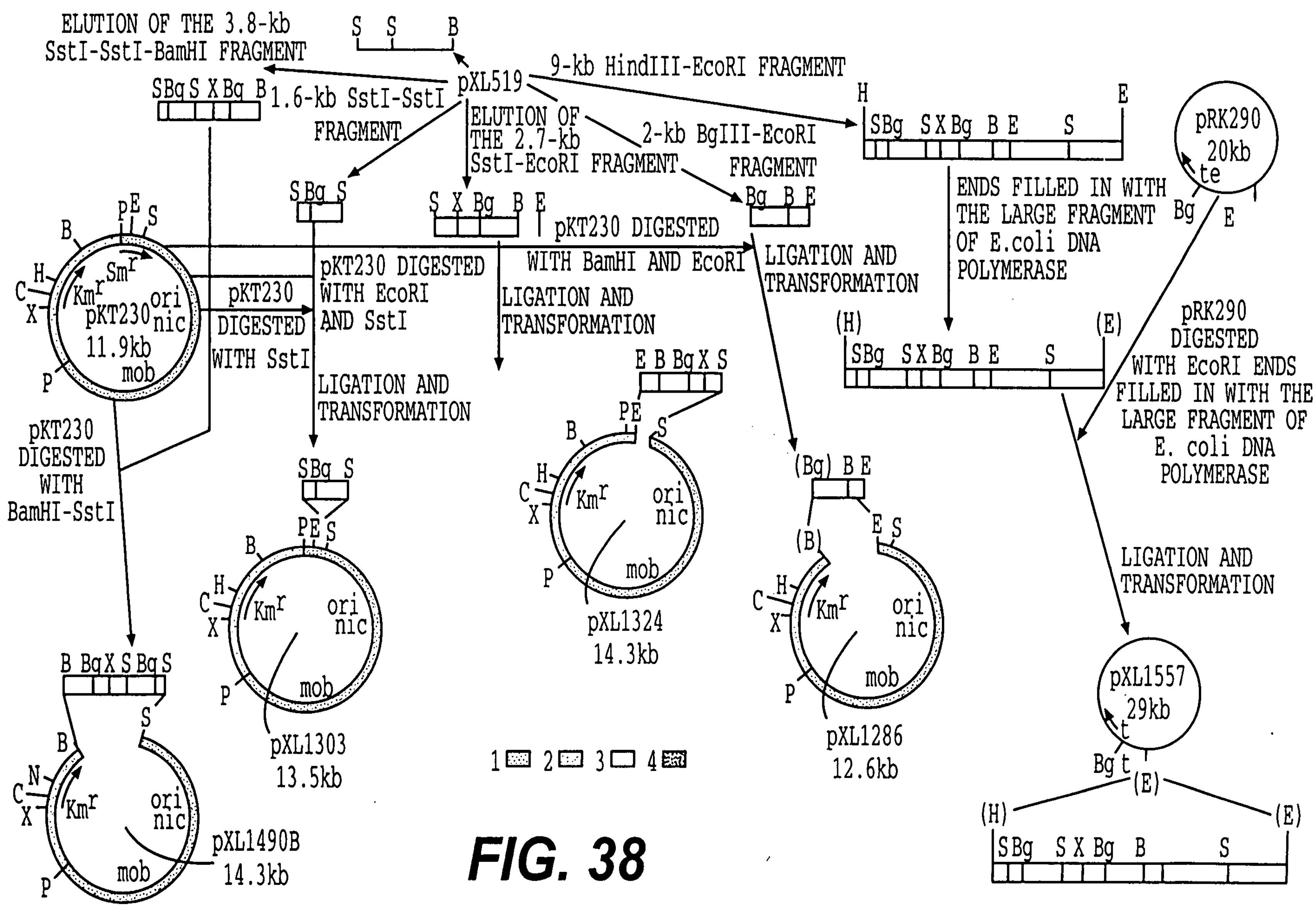

ELUTION OF THE 3.8-kb SstI-SstI-BamHI FRAGMENT
pXL519
9-kb HindIII-EcoRI FRAGMENT
1.6-kb SstI-SstI FRAGMENT
ELUTION OF THE 2.7-kb SstI-EcoRI FRAGMENT
2-kb BglII-EcoRI FRAGMENT
pKT230 11.9kb
pKT230 DIGESTED WITH BamHI AND EcoRI
pKT230 DIGESTED WITH EcoRI AND SstI
pKT230 DIGESTED WITH SstI
pKT230 DIGESTED WITH BamHI-SstI
LIGATION AND TRANSFORMATION
ENDS FILLED IN WITH THE LARGE FRAGMENT OF E.coli DNA POLYMERASE
pRK290 20kb
pRK290 DIGESTED WITH EcoRI ENDS FILLED IN WITH THE LARGE FRAGMENT OF E. coli DNA POLYMERASE
pXL1490B 14.3kb
pXL1303 13.5kb
pXL1324 14.3kb
pXL1286 12.6kb
pXL1557 29kb
1 2 3 4

FIG. 38

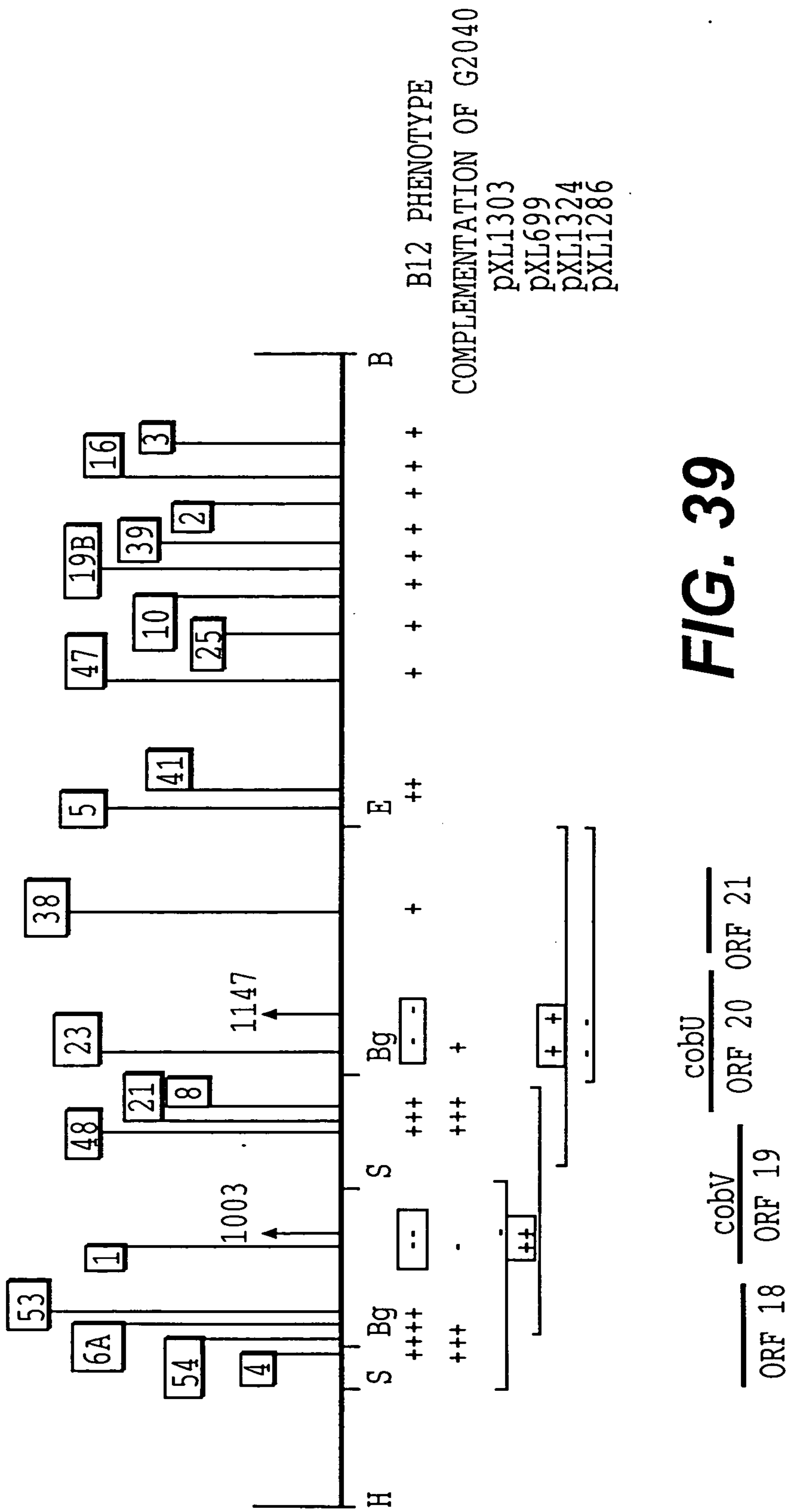

1 kb
B12 PHENOTYPE
COMPLEMENTATION OF G2040
pXL1303
pXL699
pXL1324
pXL1286
H
S
Bg
S
Bg
E
B
53
6A
54
4
1
1003
48
21
8
23
1147
38
5
41
47
25
10
19B
39
2
16
3
cobV
cobU
ORF 18
ORF 19
ORF 20
ORF 21

FIG. 39

NAME = COBS

FIRST RESIDUE = 1
LAST RESIDUE = 332

			NUMBER	NO. %	WEIGHT	WEIGHT %
1	PHE	F	15	4.52	2206.03	5.97
2	LEU	L	29	8.73	3279.44	8.87
3	ILE	I	20	6.02	2261.68	6.12
4	MET	M	7	2.11	917.28	2.48
5	VAL	V	33	9.94	3269.26	8.85
6	SER	S	15	4.52	1305.48	3.53
7	PRO	P	11	3.31	1067.58	2.89
8	THR	T	24	7.23	2425.14	6.56
9	ALA	A	32	9.64	2273.19	6.15
10	TYR	Y	9	2.71	1467.57	3.97
11	*	*	0	0.00	0.00	0.00
12	HIS	H	10	3.01	1370.59	3.71
13	GLN	Q	10	3.01	1280.59	3.46
14	ASN	N	12	3.61	1368.52	3.70
15	LYS	K	13	3.92	1665.23	4.51
16	ASP	D	28	8.43	3220.75	8.71
17	GLU	E	15	4.52	1935.64	5.24
18	CYS	C	3	0.90	309.03	0.84
19	TRP	W	4	1.20	744.32	2.01
20	ARG	R	22	6.63	3434.22	9.29
21	GLY	G	20	6.02	1140.43	3.09
22	-	-	0	0.00	0.00	0.00

RESIDUES = 332
MOLECULAR WEIGHT (MONOISOTOPIC) = 36960.0000
MOLECULAR WEIGHT (AVERAGE) = 36983.1797
INDEX OF POLARITY (%) = 44.88
ISOELECTRIC POINT = 6.34
OD 260 (1 mg/ml) = 0.611 OD 280 (1 mg/ml) = 0.891

HYDROPHILICITY
COBS FROM 1 TO 332

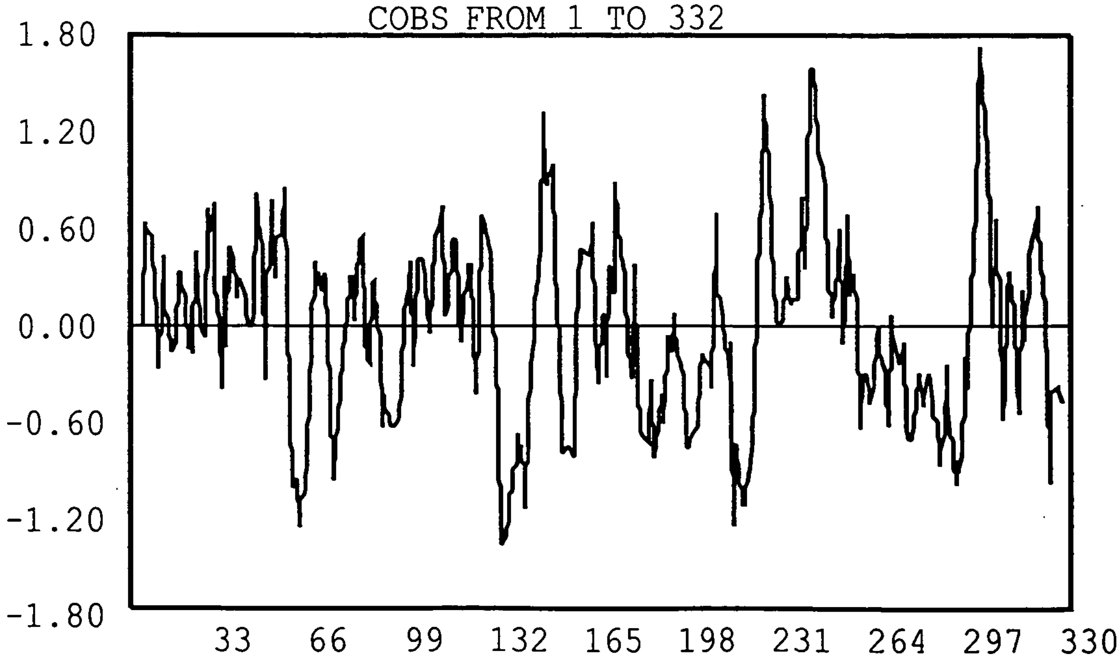


FIG. 40A

cobS GENE (SEQ ID NO: 31) AND COBS PROTEIN (SEQ ID NO: 32)
SEQUENCE OF THE 4749-BP SalI-SalI-SalI-SalI-SalI-BglI FRAGMENT
FROM 1512 TO 2510

```
MetMetSerLysIleAspLeuAspIleSerAsnLeuProAspThrThrIleSerValArgGluValPheGlyIle
ATGATGAGCAAGATTGACCTCGACATTTCCAACCTCCCCGACACCACGATTTCCGTCCGGGAGGTTTTCGGTATT
      1521      1531      1541      1551      1561      1571      1581
AspThrAspLeuArgValProAlaTyrSerLysGlyAspAlaTyrValProAspLeuAspProAspTyrLeuPhe
GATACGGATTTGCGCGTTCCTGCCTATTCGAAGGGCGACGCCTATGTCCCGGATCTGGATCCGGACTACCTCTTC
      1596      1606      1616      1626      1636      1646      1656
AspArgGluThrThrLeuAlaIleLeuAlaGlyPheAlaHisAsnArgArgValMetValSerGlyTyrHisGly
GACCGCGAAACGACGCTCGCCATTCTCGCAGGCTTCGCCCACAACCGACGCGTGATGGTGTCGGGCTATCACGGC
      1671      1681      1691      1701      1711      1721      1731
ThrGlyLysSerThrHisIleGluGlnValAlaAlaArgLeuAsnTrpProCysValArgValAsnLeuAspSer
ACCGGCAAGTCCACCCATATCGAGCAGGTCGCCGCGCGCCTCAACTGGCCGTGCGTGCGCGTCAACCTCGATAGC
      1746      1756      1766      1776      1786      1796      1806
HisValSerArgIleAspLeuValGlyLysAspAlaIleValValLysAspGlyLeuGlnValThrGluPheLys
CATGTCAGCCGTATCGACCTCGTCGGCAAGGACGCGATCGTCGTCAAGGACGGCCTGCAGGTCACCGAATTCAAG
      1821      1831      1841      1851      1861      1871      1881
AspGlyIleLeuProTrpAlaTyrGlnHisAsnValAlaLeuValPheAspGluTyrAspAlaGlyArgProAsp
GACGGCATCCTGCCCTGGGCCTACCAGCACAATGTCGCGCTCGTCTTCGACGAATACGATGCCGGCCGCCCGGAC
      1896      1906      1916      1926      1936      1946      1956
ValMetPheValIleGlnArgValLeuGluSerSerGlyArgLeuThrLeuLeuAspGlnSerArgValIleArg
GTCATGTTCGTCATCCAGCGCGTGCTGGAATCCTCCGGCCGCCTGACGCTGCTCGACCAGAGCCGTGTCATCCGT
      1971      1981      1991      2001      2011      2021      2031
ProHisProAlaPheArgLeuPheAlaThrAlaAsnThrValGlyLeuGlyAspThrThrGlyLeuTyrHisGly
CCGCACCCGGCCTTCCGCCTGTTTGCGACCGCCAACACCGTCGGCCTCGGCGACACGACCGGCCTCTATCACGGC
      2046      2056      2066      2076      2086      2096      2106
ThrGlnGlnIleAsnGlnAlaGlnMetAspArgTrpSerIleValThrThrLeuAsnTyrLeuProHisAspLys
ACGCAGCAGATCAACCAGGCGCAGATGGACCGCTGGTCGATCGTCACCACGCTGAACTACCTGCCGCACGACAAG
      2121      2131      2141      2151      2161      2171      2181
GluValAspIleValAlaAlaLysValLysGlyPheThrAlaAspLysGlyArgGluThrValSerLysMetVal
GAAGTCGACATCGTCGCCGCCAAGGTCAAGGGCTTCACCGCCGACAAGGGCCGCGAGACCGTCTCCAAGATGGTA
      2196      2206      2216      2226      2236      2246      2256
ArgValAlaAspLeuThrArgAlaAlaPheIleAsnGlyAspLeuSerThrValMetSerProArgThrValIle
CGTGTCGCCGACCTCACGCGCGCAGCCTTCATCAATGGCGATCTCTCGACTGTCATGAGCCCGCGTACGGTCATC
      2271      2281      2291      2301      2311      2321      2331
ThrTrpAlaGluAsnAlaHisIlePheGlyAspIleAlaPheAlaPheArgValThrPheLeuAsnLysCysAsp
ACCTGGGCCGAGAACGCCCACATCTTCGGCGACATCGCTTTCGCCTTCCGCGTGACCTTCCTCAACAAGTGCGAC
      2346      2356      2366      2376      2386      2396      2406
GluLeuGluArgAlaLeuValAlaGluHisTyrGlnArgAlaPheGlyIleGluLeuLysGluCysAlaAlaAsn
GAGCTGGAGCGGGCGCTGGTCGCCGAGCACTACCAGCGCGCCTTCGGCATCGAGCTGAAGGAATGCGCTGCCAAC
      2421      2431      2441      2451      2461      2471      2481
IleValLeuGluAlaThrAla***
ATCGTGCTCGAAGCCACCGCCTGA
      2496      2506
```

FIG. 40B

NAME = COBT

FIRST RESIDUE = 1
LAST RESIDUE = 631

			NUMBER	NO. %	WEIGHT	WEIGHT %
1	PHE	F	16	2.54	2353.09	3.35
2	LEU	L	56	8.87	6332.71	9.01
3	ILE	I	29	4.60	3279.44	4.67
4	MET	M	18	2.85	2358.73	3.36
5	VAL	V	31	4.91	3071.12	4.37
6	SER	S	33	5.23	2872.06	4.09
7	PRO	P	24	3.80	2329.27	3.31
8	THR	T	28	4.44	2829.34	4.03
9	ALA	A	75	11.89	5327.78	7.58
10	TYR	Y	8	1.27	1304.51	1.86
11	*	*	0	0.00	0.00	0.00
12	HIS	H	7	1.11	959.41	1.36
13	GLN	Q	29	4.60	3713.70	5.28
14	ASN	N	22	3.49	2508.94	3.57
15	LYS	K	25	3.96	3202.37	4.56
16	ASP	D	49	7.77	5636.32	8.02
17	GLU	E	67	10.62	8645.85	12.30
18	CYS	C	5	0.79	515.05	0.73
19	TRP	W	6	0.95	1116.48	1.59
20	ARG	R	61	9.67	9522.17	13.55
21	GLY	G	42	6.66	2394.90	3.41
22	-	-	0	0.00	0.00	0.00

RESIDUES = 631
MOLECULAR WEIGHT (MONOISOTOPIC) = 70291.3984
MOLECULAR WEIGHT (AVERAGE) = 70334.7656
INDEX OF POLARITY (%) = 50.87
ISOELECTRIC POINT = 5.10
OD 260 (1mg/ml) = 0.423 OD 280 (1mg/ml) = 0.610

HYDROPHILICITY
COBT FROM 1 TO 631

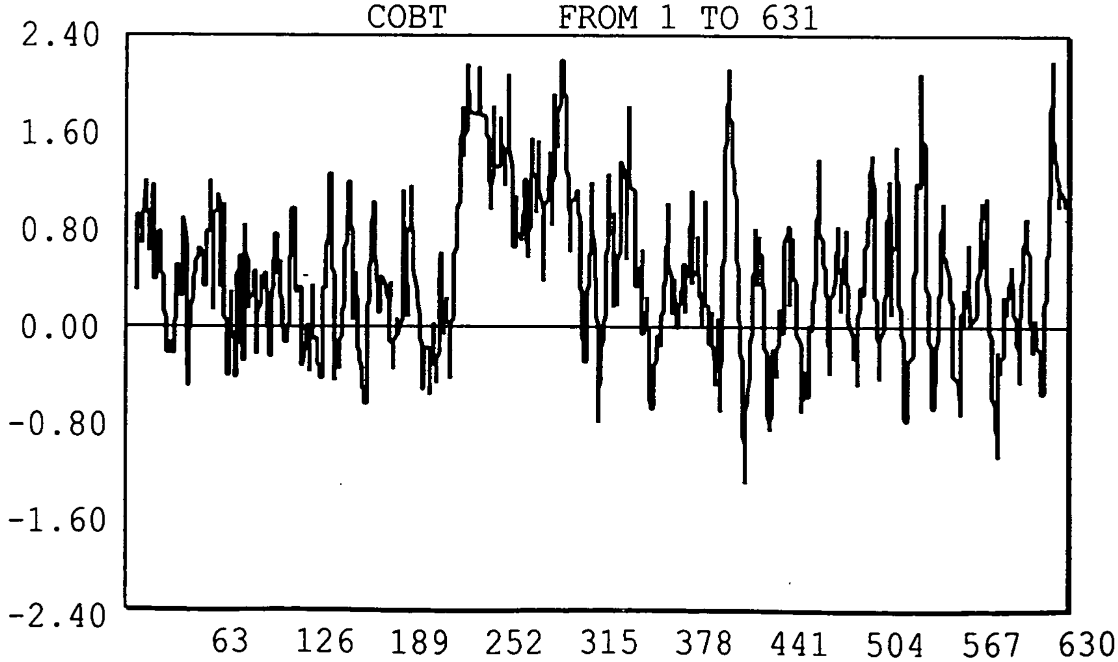


FIG. 40C

cobT GENE (SEQ ID NO: 33) AND COBT PROTEIN (SEQ ID NO: 44)
SEQUENCE OF THE 4749-BP SalI-SalI-SalI-SalI-SalI-BglI FRAGMENT
FROM 2616 TO 4511

```
ValSerSerAsnSerLysAlaLysProThrThrArgGluAsnAlaAlaGluProPheLysArgAlaLeuSerGly
GTGAGCTCGAATTCGAAGGCAAAGCCAACCACGCGCGAGAATGCTGCGGAACCGTTCAAGCGGGCGCTTTCCGGC
        2625      2635      2645      2655      2665      2675      2685
CysIleArgSerIleAlaGlyAspAlaGluValGluValAlaPheAlaAsnGluArgProGlyMetThrGlyGlu
TGCATCCGATCGATCGCGGGCGATGCCGAGGTGGAAGTCGCCTTCGCCAACGAGCGGCCGGGCATGACCGGCGAA
        2700      2710      2720      2730      2740      2750      2760
ArgIleArgLeuProGluLeuSerLysArgProThrLeuGlnGluLeuAlaValThrArgGlyLeuGlyAspSer
CGCATCCGTCTGCCGGAACTTTCCAAGCGCCCGACCCTGCAGGAACTTGCCGTGACCCGCGGGCTCGGTGACAGC
        2775      2785      2795      2805      2815      2825      2835
MetAlaLeuArgLysAlaCysThrHisAlaArgIleGlnArgThrMetSerProGlnGlyAlaAspAlaArgAla
ATGGCGCTGCGCAAGGCCTGTACGCATGCGCGGATCCAGCGCACCATGTCGCCGCAAGGGGCGGACGCCCGCGCG
        2850      2860      2870      2880      2890      2900      2910
IlePheAspAlaValGluGlnAlaArgValGluAlaIleGlySerLeuArgMetAlaGlyValAlaLysAsnLeu
ATCTTCGATGCGGTGGAGCAGGCTCGTGTCGAGGCGATCGGGTCGTTGCGCATGGCGGGTGTCGCCAAGAACCTC
        2925      2935      2945      2955      2965     2975      2985
AsnValMetLeuGluGluLysTyrAlaLysAlaAsnPheAlaThrIleGluArgGlnAlaAspAlaProLeuGly
AACGTCATGCTCGAAGAGAAATACGCCAAGGCGAATTTCGCAACGATCGAGCGCCAGGCGGACGCGCCGCTCGGC
        3000      3010      3020      3030      3040      3050      3060
GluAlaValAlaLeuLeuValArgGluLysLeuThrGlyGlnLysProProAlaSerAlaGlyLysValLeuAsp
GAGGCCGTAGCGCTGCTGGTGCGCGAGAAGCTGACGGGCCAGAAGCCGCCGGCGTCTGCCGGCAAGGTGCTCGAC
        3075      3085      3095      3105      3115      3125      3135
LeuTrpArgGluPheIleGluGlyLysAlaAlaGlyAspIleGluHisLeuSerSerThrIleAsnAsnGlnGln
CTCTGGCGCGAGTTCATCGAGGGCAAGGCTGCCGGCGACATTGAGCACCTGTCGTCGACGATCAACAACCAGCAG
        3150      3160      3170      3180      3190      3200      3210
AlaPheAlaArgValValArgAspMetLeuThrSerMetGluValAlaGluLysTyrGlyAspAspAspAsnGlu
GCCTTTGCCCGGGTCGTTCGCGACATGCTGACCTCGATGGAAGTCGCCGAGAAATACGGTGACGACGACAACGAG
        3225      3235      3245      3255      3265      3275      3285
ProAspGluGlnGluSerGluThrAspGluAspGlnProArgSerGlnGluGlnAspGluAsnAlaSerAspGlu
CCGGACGAGCAGGAAAGCGAGACCGACGAAGACCAGCCGCGCAGCCAGGAGCAGGACGAGAACGCCAGCGACGAG
        3300      3310      3320      3330      3340      3350      3360
GluAlaGlyAspAspAlaAlaProAlaAspGluAsnGlnAlaAlaGluGluGlnMetGluGluGlyGluMetAsp
GAAGCCGGCGACGATGCCGCACCCGCCGACGAGAACCAGGCTGCCGAAGAGCAGATGGAAGAAGGCGAGATGGAC
        3375      3385      3395      3405      3415      3425      3435
GlyAlaGluIleSerAspAspAspLeuGlnAspGluGlyAspGluAspSerGluThrProGlyGluValLysArg
GGCGCGGAGATCTCCGACGACGATCTCCAGGACGAAGGCGACGAGGACAGCGAAACGCCCGGCGAGGTCAAGCGT
        3450      3460      3470      3480      3490      3500      3510
```

FIG. 40D

```
ProAsnGlnProPheAlaAspPheAsnGluLysValAspTyrAlaValPheThrArgGluPheAspGluThrIle
CCGAACCAGCCCTTCGCCGACTTCAACGAGAAGGTCGACTACGCCGTCTTCACCCGCGAGTTCGACGAGACGATT
       3525      3535      3545      3555      3565      3575      3585
AlaSerGluGluLeuCysAspGluAlaGluLeuAspArgLeuArgAlaPheLeuAspLysGlnLeuAlaHisLeu
GCCTCGGAAGAGCTTTGCGACGAGGCCGAGCTCGACCGGCTGCGCGCCTTCCTCGACAAGCAGCTTGCCCATCTT
       3600      3610      3620      3630      3640      3650      3660
GlnGlyAlaValGlyArgLeuAlaAsnArgLeuGlnArgArgLeuMetAlaGlnGlnAsnArgSerTrpGluPhe
CAAGGCGCGGTCGGCCGCCTTGCCAACCGGCTGCAGCGCCGCCTGATGGCGCAGCAGAACCGCTCCTGGGAGTTC
       3675      3685      3695      3705      3715      3725      3735
AspLeuGluGluGlyTyrLeuAspSerAlaArgLeuGlnArgIleIleIleAspProMetGlnProLeuSerPhe
GATCTCGAAGAGGGGTATCTCGATTCGGCGCGGCTTCAGCGCATCATCATCGATCCGATGCAGCCGCTTTCCTTC
       3750      3760      3770      3780      3790      3800      3810
LysArgGluLysAspThrAsnPheArgAspThrValValThrLeuLeuIleAspAsnSerGlySerMetArgGly
AAGCGCGAAAAGGACACCAACTTCCGCGATACCGTCGTGACGCTGCTGATCGACAATTCCGGCTCGATGCGCGGC
       3825      3835      3845      3855      3865      3875      3885
ArgProIleThrValAlaAlaThrCysAlaAspIleLeuAlaArgThrLeuGluArgCysGlyValLysValGlu
CGTCCGATCACGGTTGCCGCCACCTGCGCCGATATCCTGGCGCGCACGCTCGAGCGCTGCGGCGTCAAGGTCGAG
       3900      3910      3920      3930      3940      3950      3960
IleLeuGlyPheThrThrLysAlaTrpLysGlyGlyGlnSerArgGluLysTrpLeuAlaGlyGlyLysProGln
ATCCTCGGTTTTACCACCAAGGCGTGGAAGGGTGGGCAGTCACGCGAGAAGTGGCTGGCCGGCGGCAAGCCACAG
       3975      3985      3995      4005      4015      4025      4035
AlaProGlyArgLeuAsnAspLeuArgHisIleValTyrLysSerAlaAspAlaProTrpArgArgAlaArgArg
GCCCCGGGTCGCCTCAACGACCTGCGACACATCGTCTACAAGTCTGCCGACGCTCCGTGGCGCCGGGCACGACGC
       4050      4060      4070      4080      4090      4100      4110
AsnLeuGlyLeuMetMetArgGluGlyLeuLeuLysGluAsnIleAspGlyGluAlaLeuIleTrpAlaHisGlu
AATCTCGGCCTGATGATGCGGGAAGGCCTGCTCAAGGAAAACATCGACGGCGAGGCGTTGATTTGGGCGCATGAG
       4125      4135      4145      4155      4165      4175      4185
ArgLeuMetAlaArgArgGluGlnArgArgIleLeuMetMetIleSerAspGlyAlaProValAspAspSerThr
CGGCTGATGGCGCGGCGCGAACAGCGGCGCATCCTGATGATGATTTCGGACGGCGCGCCGGTCGACGACTCGACG
       4200      4210      4220      4230      4240      4250      4260
LeuSerValAsnProGlyAsnTyrLeuGluArgHisLeuArgAlaValIleGluGlnIleGluThrArgSerPro
CTGTCGGTCAATCCAGGAAACTATCTGGAGCGTCACCTGCGCGCGGTCATCGAGCAGATCGAAACGCGCTCGCCG
       4275      4285      4295      4305      4315      4325      4335
ValGluLeuLeuAlaIleGlyIleGlyHisAspValThrArgTyrTyrArgArgAlaValThrIleValAspAla
GTGGAACTGCTGGCGATCGGTATCGGCCACGACGTGACGCGCTACTATCGCCGTGCCGTCACCATCGTCGATGCC
       4350      4360      4370      4380      4390      4400      4410
AspGluLeuAlaGlyAlaMetThrGluGlnLeuAlaAlaLeuPheGluAspGluSerGlnArgArgGlySerSer
GATGAGCTTGCCGGCGCGATGACCGAACAGCTGGCCGCACTCTTCGAGGACGAAAGCCAGCGCCGCGGTTCTTCG
       4425      4435      4445      4455      4465      4475      4485
ArgLeuArgArgAlaGly***
CGTCTTCGCCGCGCCGGGTGA
       4500      4510
```

FIG. 40E

NAME = COBX

FIRST RESIDUE = 1
LAST RESIDUE = 93

			NUMBER	NO. %	WEIGHT	WEIGHT %
1	PHE	F	3	3.23	441.21	4.29
2	LEU	L	8	8.60	904.67	8.80
3	ILE	I	5	5.38	565.42	5.50
4	MET	M	3	3.23	393.12	3.82
5	VAL	V	5	5.38	495.34	4.82
6	SER	S	6	6.45	522.19	5.08
7	PRO	P	6	6.45	582.32	5.66
8	THR	T	5	5.38	505.24	4.92
9	ALA	A	10	10.75	710.37	6.91
10	TYR	Y	0	0.00	0.00	0.00
11	*	*	0	0.00	0.00	0.00
12	HIS	H	7	7.53	959.41	9.33
13	GLN	Q	2	2.15	256.12	2.49
14	ASN	N	2	2.15	228.09	2.22
15	LYS	K	3	3.23	384.28	3.74
16	ASP	D	3	3.23	345.08	3.36
17	GLU	E	10	10.75	1290.43	12.55
18	CYS	C	0	0.00	0.00	0.00
19	TRP	W	1	1.08	186.08	1.81
20	ARG	R	7	7.53	1092.71	10.63
21	GLY	G	7	7.53	399.15	3.88
22	-	-	0	0.00	0.00	0.00

RESIDUES = 93
MOLECULAR WEIGHT (MONOISOTOPIC) = 10279.2354
MOLECULAR WEIGHT (AVERAGE) = 10285.6309
INDEX OF POLARITY (%) = 48.39
ISOELECTRIC POINT = 6.94
OD 260 (1mg/ml) = 0.411 OD 280 (1mg/ml) = 0.541

HYDROPHILICITY
COBX FROM 1 TO 93

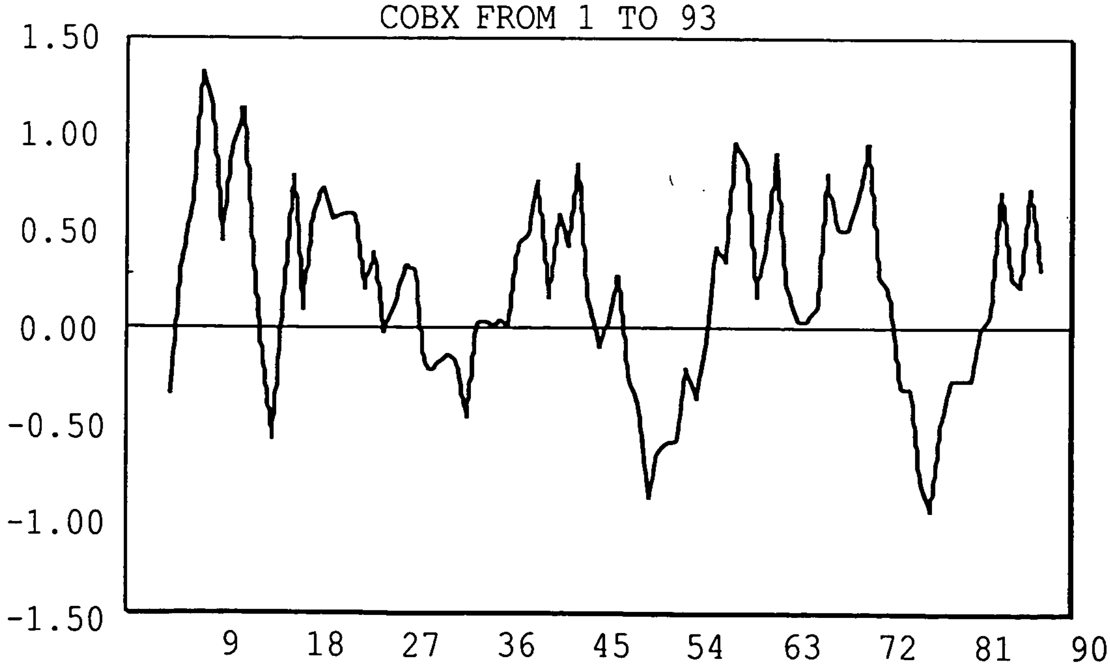


FIG. 40F

cobX GENE (SEQ ID NO: 35) AND COBX PROTEIN (SEQ ID NO: 36)
SEQUENCE OF THE 4749-BP BglI-SalI-SalI-SalI-SalI-SalI FRAGMENT
FROM 4089 TO 4370

```
MetSerLeuThrGluThrIleGluLysLysLeuIleGluAlaPheHisProGluArgLeuGluValIleAsnGlu
ATGTCGCTCACCGAGACCATCGAAAAGAAGCTGATCGAGGCCTTCCACCCTGAACGGCTCGAGGTCATCAACGAG
      4098      4108      4118      4128      4138      4148      4158
SerHisGlnHisThrGlyHisGlnProGlyPheAspGlyThrGlyGluSerHisMetArgValArgIleValSer
AGCCATCAGCATACCGGCCATCAGCCGGGCTTCGATGGTACCGGCGAGTCCCACATGCGGGTGCGTATCGTTTCT
      4173      4183      4193      4203      4213      4223      4233
SerAlaPheAlaGlyMetSerArgValAlaArgHisArgAlaIleAsnAspLeuLeuLysProGluLeuAspAla
AGCGCCTTTGCCGGCATGAGCCGTGTCGCCCGCCACCGCGCCATCAATGATCTCCTGAAGCCAGAACTCGACGCC
      4248      4258      4268      4278      4288      4298      4308
GlyLeuHisAlaLeuAlaValGluProAlaAlaProGlyGluProThrArgTrp**
GGCCTGCATGCGCTCGCCGTCGAGCCGGCAGCCCCCGGCGAGCCGACCCGCTGGTAG
      4323      4333      4343      4353      4363
```

FIG. 40G

NAME = COBU

FIRST RESIDUE = 1
LAST RESIDUE = 338

			NUMBER	NO. %	WEIGHT	WEIGHT %
1	PHE	F	9	2.66	1323.62	3.82
2	LEU	L	36	10.65	4071.03	11.75
3	ILE	I	19	5.62	2148.60	6.20
4	MET	M	9	2.66	1179.36	3.40
5	VAL	V	21	6.21	2080.44	6.00
6	SER	S	13	3.85	1131.42	3.26
7	PRO	P	16	4.73	1552.84	4.48
8	THR	T	17	5.03	1717.81	4.96
9	ALA	A	61	18.05	4333.26	12.50
10	TYR	Y	3	0.89	489.19	1.41
11	*	*	0	0.00	0.00	0.00
12	HIS	H	8	2.37	1096.47	3.16
13	GLN	Q	6	1.78	768.35	2.22
14	ASN	N	9	2.66	1026.39	2.96
15	LYS	K	12	3.55	1537.14	4.43
16	ASP	D	13	3.85	1495.35	4.31
17	GLU	E	22	6.51	2838.94	8.19
18	CYS	C	5	1.48	515.05	1.49
19	TRP	W	3	0.89	558.24	1.61
20	ARG	R	16	4.73	2497.62	7.21
21	GLY	G	40	11.83	2280.86	6.58
22	-	-	0	0.00	0.00	0.00

RESIDUES = 338
MOLECULAR WEIGHT (MONOISOTOPIC) = 34659.9844
MOLECULAR WEIGHT (AVERAGE) = 34681.9609
INDEX OF POLARITY (%) = 34.32
ISOELECTRIC POINT = 6.21
OD 260 (1mg/ml) = 0.416 OD 280 (1mg/ml) = 0.584

HYDROPHILICITY
COBU FROM 1 TO 338

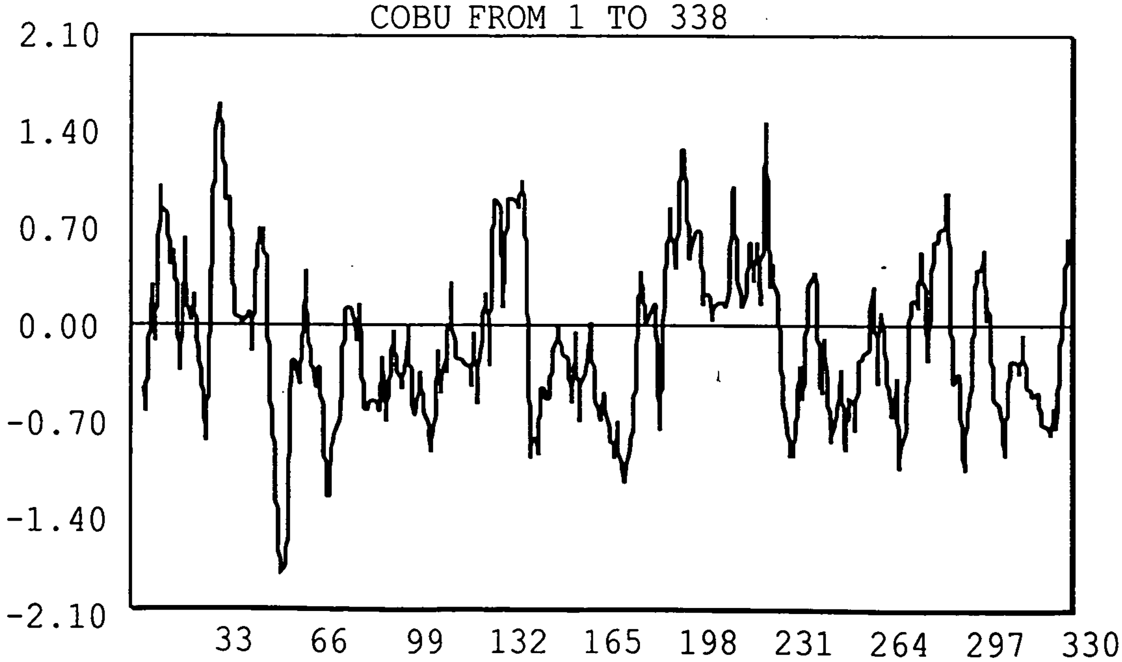


FIG. 41A

cobU GENE (SEQ ID NO: 37) AND COBU PROTEIN (SEQ ID NO: 38)
SEQUENCE OF THE 3855-BP SstI-SstI-BamHI FRAGMENT
FROM 2099 TO 3115

```
MetSerAlaSerGlyLeuProPheAspAspPheArgGluLeuLeuArgAsnLeuProGlyProAspAlaAlaAla
ATGAGTGCCAGCGGCCTGCCGTTTGATGATTTCGCGAATTGTTGCGCAACCTGCCGGGCCCGGATGCGGCAGCC
      2108      2118      2128      2138      2148      2158      2168
LeuValAlaAlaArgGluArgAspAlaGlnLeuThrLysProProGlyAlaLeuGlyArgLeuGluGluIleAla
CTCGTTGCCGCGCGGGAGCGGGACGCCCAGCTGACGAAGCCGCCGGGCGCGCTCGGCCGCCTCGAGGAAATCGCC
      2183      2193      2203      2213      2223      2233      2243
PheTrpLeuAlaAlaTrpThrGlyLysAlaProValValAsnArgProLeuValAlaIlePheAlaGlyAsnHis
TTCTGGCTCGCCGCCTGGACGGGCAAGGCGCCGGTGGTCAACCGGCCGCTGGTGGCGATCTTTGCCGGCAACCAC
      2258      2268      2278      2288      2298      2308      2318
GlyValThrArgGlnGlyValThrProPheProSerSerValThrAlaGlnMetValGluAsnPheAlaAlaGly
GGCGTCACCCGCCAGGGGGTGACCCCGTTCCCGTCATCCGTCACCGCACAGATGGTCGAGAATTTTGCCGCCGGT
      2333      2343      2353      2363      2373      2383      2393
GlyAlaAlaIleAsnGlnIleCysValSerHisAspLeuGlyLeuLysValPheAspLeuAlaLeuGluTyrPro
GGCGCTGCGATCAACCAGATCTGCGTCAGCCACGACCTCGGGCTGAAGGTCTTCGACCTCGCACTCGAATACCCG
      2408      2418      2428      2438      2448      2458      2468
ThrGlyAspIleThrGluGluAlaAlaLeuSerGluArgAspCysAlaAlaThrMetAlaPheGlyMetGluAla
ACCGGTGATATCACCGAGGAAGCCGCGCTGTCCGAGCGCGATTGCGCCGCGACCATGGCCTTTGGCATGGAGGCG
      2483      2493      2503      2513      2523      2533      2543
IleAlaGlyGlyThrAspLeuLeuCysIleGlyGluMetGlyIleGlyAsnThrThrIleAlaAlaAlaIleAsn
ATTGCCGGCGGCACGGATCTTCTGTGCATCGGCGAAATGGGCATCGGCAACACCACGATCGCGGCCGCGATCAAT
      2558      2568      2578      2588      2598      2608      2618
LeuGlyLeuTyrGlyGlyThrAlaGluGluTrpValGlyProGlyThrGlySerGluGlyGluValLeuLysArg
CTCGGCCTTTATGGTGGCACGGCCGAAGAATGGGTCGGTCCGGGTACCGGCTCCGAGGGCGAGGTGCTGAAGCGC
      2633      2643      2653      2663      2673      2683      2693
LysIleAlaAlaValGluLysAlaValAlaLeuHisArgAspHisLeuSerAspProLeuGluLeuMetArgArg
AAGATCGCCGCGGTCGAAAAGGCCGTGGCGCTGCATCGCGATCACCTGTCCGATCCGCTCGAACTGATGCGTCGC
      2708      2718      2728      2738      2748      2758      2768
LeuGlyGlyArgGluIleAlaAlaMetAlaGlyAlaIleLeuAlaAlaArgValGlnLysValProValIleIle
CTCGGCGGTCGTGAGATCGCGGCCATGGCTGGCGCCATCCTGGCCGCCCGCGTCCAGAAGGTACCTGTCATCATC
      2783      2793      2803      2813      2823      2833      2843
AspGlyTyrValAlaThrAlaAlaAlaSerIleLeuLysAlaAlaAsnProSerAlaLeuAspHisCysLeuIle
GACGGCTACGTGGCGACCGCTGCGGCTTCGATCCTGAAGGCGGCCAACCCGTCGGCCCTCGACCATTGCCTGATC
      2858      2868      2878      2888      2898      2908      2918
GlyHisValSerGlyGluProGlyHisLeuArgAlaIleGluLysLeuGlyLysThrProLeuLeuAlaLeuGly
GGCCATGTTTCGGGCGAACCGGGGCATCTGCGCGCGATCGAGAAGCTCGGCAAGACGCCGCTGCTGGCACTCGGC
      2933      2943      2953      2963      2973      2983      2993
MetArgLeuGlyGluGlyThrGlyAlaAlaLeuAlaAlaGlyIleValLysAlaAlaAlaAlaCysHisSerGly
ATGCGGCTTGGCGAAGGCACGGGCGCGGCCCTTGCCGCCGGTATCGTCAAGGCGGCGGCCGCTTGCCACAGCGGC
      3008      3018      3028      3038      3048      3058      3068
MetAlaThrPheAlaGlnAlaGlyValSerAsnLysGlu***
ATGGCGACCTTTGCCCAGGCCGGCGTCAGCAACAAGGAATAG
      3083      3093      3103      3113
```

FIG. 41B

NAME = COBV

FIRST RESIDUE = 1
LAST RESIDUE = 302

			NUMBER	NO. %	WEIGHT	WEIGHT %
1	PHE	F	18	5.96	2647.23	8.64
2	LEU	L	39	12.91	4410.28	14.39
3	ILE	I	13	4.30	1470.09	4.80
4	MET	M	10	3.31	1310.41	4.28
5	VAL	V	23	7.62	2278.57	7.44
6	SER	S	18	5.96	1566.58	5.11
7	PRO	P	12	3.97	1164.63	3.80
8	THR	T	10	3.31	1010.48	3.30
9	ALA	A	63	20.86	4475.34	14.61
10	TYR	Y	3	0.99	489.19	1.60
11	*	*	0	0.00	0.00	0.00
12	HIS	H	3	0.99	411.18	1.34
13	GLN	Q	6	1.99	768.35	2.51
14	ASN	N	2	0.66	228.09	0.74
15	LYS	K	5	1.66	640.47	2.09
16	ASP	D	10	3.31	1150.27	3.75
17	GLU	E	7	2.32	903.30	2.95
18	CYS	C	3	0.99	309.03	1.01
19	TRP	W	2	0.66	372.16	1.21
20	ARG	R	19	6.29	2965.92	9.68
21	GLY	G	36	11.92	2052.77	6.70
22	-	-	0	0.00	0.00	0.00

RESIDUES = 302
MOLECULAR WEIGHT (MONOISOTOPIC) = 30642.3359
MOLECULAR WEIGHT (AVERAGE) = 30662.0820
INDEX OF POLARITY (%) = 26.49
ISOELECTRIC POINT = 9.97
OD 260 (1mg/ml) = 0.391 OD 280 (1mg/ml) = 0.479

HYDROPHILICITY
COBV FROM 1 TO 302

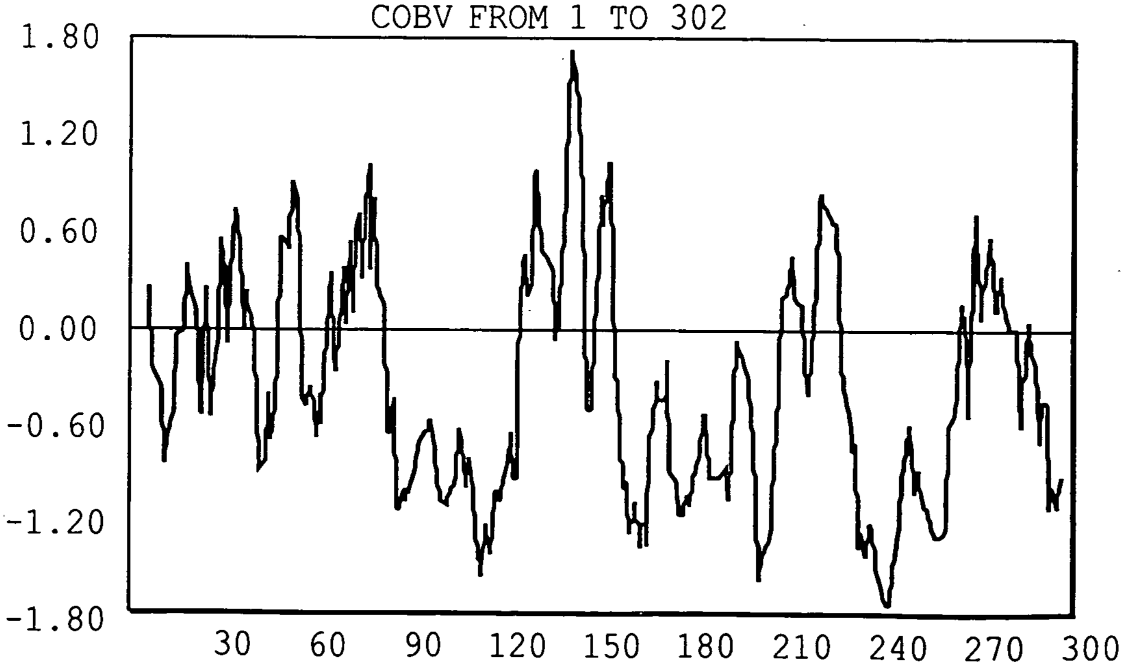


FIG. 41C

cobV GENE (SEQ ID NO: 39) AND COBV PROTEIN (SEQ ID NO: 40)
SEQUENCE OF THE 3855-BP BamHI-SstI-SstI FRAGMENT
FROM 1885 TO 2793

```
MetLysGlyLeuGlyLysValCysAlaAlaLeuAlaGlyAlaProAlaArgLeuAlaArgLeuAlaAlaValGly
ATGAAAGGTCTGGGAAAAGTGTGCGCGGCCCTCGCGGGTGCGCCCGCCCGGCTTGCGAGACTCGCCGCAGTCGGC
      1894      1904      1914      1924      1934      1944      1954
GluPheGlySerGlyArgValAsnGlyArgAsnLeuGlyGlyAlaMetGlyPheValGlyAspPheCysAspAsp
GAGTTTGGCAGCGGCCGGGTCAATGGCCGCAACCTTGGAGGAGCCATGGGCTTCGTTGGCGATTTCTGTGACGAT
      1969      1979      1989      1999      2009      2019      2029
ValAlaArgSerIleGlyPheLeuSerArgIleProMetProAlaArgHisPheGluGlyTyrAspGlyArgLeu
GTGGCGCGGTCGATCGGCTTTCTCAGCCGCATCCCGATGCCTGCGCGTCATTTCGAAGGTTATGACGGGCGCTTG
      2044      2054      2064      2074      2084      2094      2104
SerArgAlaValArgAlaPheProPheAlaGlyLeuAlaIleAlaLeuProSerAlaAlaValAlaMetAlaLeu
AGCCGTGCCGTGCGCGCCTTCCCGTTCGCCGGCCTGGCGATCGCACTGCCATCGGCGGCCGTCGCCATGGCCCTC
      2119      2129      2139      2149      2159      2169      2179
MetAlaLeuGlnValSerSerLeuPheAlaAlaPheValValValAlaIleGlnAlaLeuValThrGlyAlaLeu
ATGGCGCTGCAGGTGAGCTCGCTCTTTGCCGCCTTTGTCGTCGTCGCCATCCAGGCGCTTGTCACCGGCGCACTG
      2194      2204      2214      2224      2234      2244      2254
HisGluAspGlyLeuGlyAspThrAlaAspGlyPheGlyGlyGlyArgAspArgGluAlaAlaLeuAlaIleMet
CACGAAGACGGGCTTGGCGACACGGCCGATGGCTTTGGCGGCGGTCGCGACCGCGAAGCGGCGCTTGCGATCATG
      2269      2279      2289      2299      2309      2319      2329
LysAspSerArgIleGlyThrTyrAlaAlaValAlaLeuIleLeuSerPheGlyLeuArgValSerAlaPheAla
AAGGACAGCCGCATCGGCACCTATGCGGCCGTCGCCCTCATCCTCTCCTTCGGCCTGCGCGTCTCGGCGTTCGCC
      2344      2354      2364      2374      2384      2394      2404
SerIleLeuProLeuPheSerProLeuGlyAlaAlaMetAlaIleLeuGlyAlaAlaCysLeuSerArgAlaAla
TCGATCCTGCCGCTCTTTTCGCCGCTGGGCGCCGCCATGGCGATCCTTGGCGCAGCGTGCCTCAGCCGCGCCGCC
      2419      2429      2439      2449      2459      2469      2479
MetValTrpHisTrpSerSerLeuProProAlaArgSerSerGlyValAlaAlaSerAlaGlyGluProGluPro
ATGGTCTGGCACTGGTCGTCGCTTCCGCCGGCGCGCAGCAGCGGCGTCGCGGCCTCGGCTGGCGAGCCGGAACCG
      2494      2504      2514      2524      2534      2544      2554
AlaAlaThrArgPheAlaLeuAlaPheGlyLeuLeuValAlaMetLeuLeuPheTyrLeuAlaGlnValProAla
GCGGCCACGCGCTTCGCGCTTGCCTTCGGACTTCTTGTCGCAATGCTGCTCTTCTATCTCGCGCAGGTCCCGGCG
      2569      2579      2589      2599      2609      2619      2629
LeuGlyValIleAlaAlaLeuValAlaPheLeuAlaThrValLysGlyPheAlaArgLeuAlaMetArgLysIle
CTCGGCGTCATCGCGGCGCTCGTCGCATTCCTTGCCACGGTCAAGGGCTTCGCTCGGCTGGCGATGCGCAAGATC
      2644      2654      2664      2674      2684      2694      2704
GlyGlyGlnThrGlyAspThrIleGlyAlaThrGlnGlnLeuThrGluIleAlaValLeuGlyAlaLeuAlaLeu
GGCGGACAAACGGGCGACACGATCGGGGCGACGCAGCAACTGACCGAAATCGCCGTGCTCGGTGCCCTTGCGCTG
      2719      2729      2739      2749      2759      2769      2779
ThrVal***
ACGGTTTGA
```

FIG. 41D

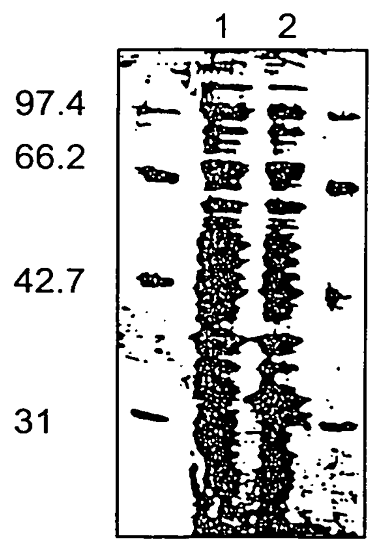


FIG. 42A

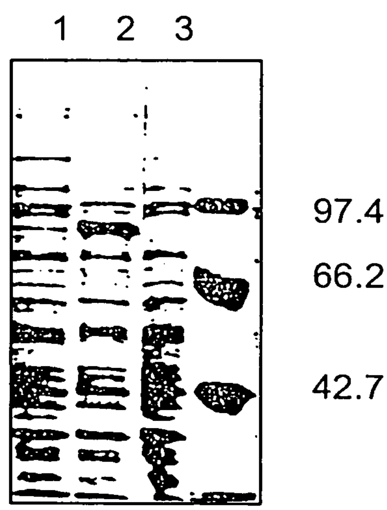


FIG. 42B

```
SEQUENCE      LENGTH = 13144 FROM      1 TO 13144
        10         20         30         40         50         60
GAGCTCGAAG GGGCTTCCGC CCCGATCGCT GGCGTTAGCC GACGTTCGAC GTGCGGATGA
CTCGAGCTTC CCCGAAGGCG GGGCTAGCGA CCGCAATCGG CTGCAAGCTG CACGCCTACT

        70         80         90        100        110        120
CGCCGAGCGG GCCGAAGGGC GCGTCGACGA CGAGGTTGCG TACGCGCGAC TGGCTGGACG
GCGGCTCGCC CGGCTTCCCG CGCAGCTGCT GCTCCAACGC ATGCGCGCTG ACCGACCTGC

       130        140        150        160        170        180
GAACCTTCGA GTTCCAGGCG ATCTGAACGA AATTGGGCTT GCTGAAAATA TACAGCATGG
CTTGGAAGCT CAAGGTCCGC TAGACTTGCT TTAACCCGAA CGACTTTTAT ATGTCGTACC

       190        200        210        220        230        240
ACATGAACCT TGAGAGGCCG GAGGCCTATC CTCCGGGGCG TGTTGCTATG CCGCTGATAT
TGTACTTGGA ACTCTCCGGC CTCCGGATAG GAGGCCCCGC ACAACGATAC GGCGACTATA

       250        260        270        280        290        300
AGGTGTGCGC TGCAAAAAAT TGAATGCCAA ACTCGCCACG CCATGTCGCA TTCTGGCTAT
TCCACACGCG ACGTTTTTTA ACTTACGGTT TGAGCGGTGC GGTACAGCGT AAGACCGATA

       310        320        330        340        350        360
CGGCCGCGAC ATTTTCGACA AGCCTTGCGA AAGCGCGAAA CAATGCGTGA AAGGGCTTTG
GCCGGCGCTG TAAAAGCTGT TCGGAACGCT TTCGCGCTTT GTTACGCACT TTCCCGAAAC

       370        380        390        400        410        420
TCAATTGCGG CGAAATCGTG TCGAAACAGA CCTTTGCCGC TGCCCGTTTC AGTGTTACCG
AGTTAACGCC GCTTTAGCAC AGCTTTGTCT GGAAACGGCG ACGGGCAAAG TCACAATGGC

       430        440        450        460        470        480
ATGGCCGCAT GACACGCAGG ATCATGTTGC AGGGAACCGG CTCGGATGTC GGAAAATCGG
TACCGGCGTA CTGTGCGTCC TAGTACAACG TCCCTTGGCC GAGCCTACAG CCTTTTAGCC

       490        500        510        520        530        540
TATTGGTGGC GGGGCTCTGC CGGCTTGCCG CCAATCAGGG CCTGAAGGTC CGGCCGTTCA
ATAACCACCG CCCCGAGACG GCCGAACGGC GGTTAGTCCC GGACTTCCAG GCCGGCAAGT

       550        560        570        580        590        600
AGCCGCAGAA CATGTCGAAC AACGCCGCCG TTTCCGACGA CGGCGGCGAC ATCGGCCGCG
TCGGCGTCTT GTACAGCTTG TTGCGGCGGC AAAGGCTGCT GCCGCCGCTC TAGCCGGCGC
```

FIG. 43A

610 620 630 640 650 660
CGCAATGGCT GCAGGCGCTG GCCGCGCGCG TGCCGTCGTC GGTGCACATG AACCCGGTGC
GCGTTACCGA CGTCCGCGAC CGGCGCGCGC ACGGCAGCAG CCACGTGTAC TTGGGCCACG

670 680 690 700 710 720
TCCTGAAGCC GCAGTCGGAC GTGGGCAGCC AGATCGTCGT TCAGGGCAAG GTCGCCGGGC
AGGACTTCGG CGTCAGCCTG CACCCGTCGG TCTAGCAGCA AGTCCCGTTC CAGCGGCCCG

730 740 750 760 770 780
AGGCCAGGGG GCGGGAATAT CAGGCGCTCA AGCCCAAGCT GCTGGGCGCC GTCATGGAGA
TCCGGTCCCC CGCCCTTATA GTCCGCGAGT TCGGGTTCGA CGACCCGCGG CAGTACCTCT

790 800 810 820 830 840
GTTTCGAACA AATATCGGCC GGTGCCGATC TCGTGGTGGT CGAAGGCGCC GGCTCGCCGG
CAAAGCTTGT TTATAGCCGG CCACGGCTAG AGCACCACCA GCTTCCGCGG CCGAGCGGCC

850 860 870 880 890 900
CCGAAATCAA CCTCAGGCCC GGCGACATCG CCAATATGGG CTTTGCGACA CGGGCCAATG
GGCTTTAGTT GGAGTCCGGG CCGCTGTAGC GGTTATACCC GAAACGCTGT GCCCGGTTAC

910 920 930 940 950 960
TGCCGGTCGT GCTGGTCGGC GACATCGACC GCGGGGGGGT GATCGCCTCG CTGGTCGGCA
ACGGCCAGCA CGACCAGCCG CTGTAGCTGG CGCCCCCCCA CTAGCGGAGC GACCAGCCGT

970 980 990 1000 1010 1020
CGCATGCGAT CCTGCCCGAG GAAGACCGGC GCATGGTGAC CGGCTATCTC ATCAACAAGT
GCGTACGCTA GGACGGGCTC CTTCTGGCCG CGTACCACTG GCCGATAGAG TAGTTGTTCA

1030 1040 1050 1060 1070 1080
TCCGCGGCGA CGTCACGCTG TTCGACGACG GCATTGCTGC CGTCAACCGC TACACCGGCT
AGGCGCCGCT GCAGTGCGAC AAGCTGCTGC CGTAACGACG GCAGTTGGCG ATGTGGCCGA

1090 1100 1110 1120 1130 1140
GGCCCTGCTT CGGCGTCGTG CCGTGGCTGA AGGCGGCGGC ACGCCTGCCG GCGGAAGATT
CCGGGACGAA GCCGCAGCAC GGCACCGACT TCCGCCGCCG TGCGGACGGC CGCCTTCTAA

1150 1160 1170 1180 1190 1200
CCGTCGTGCT GGAGAAGCTG ACGCGCGGCG AGGGGCGGGC GCTGAAGGTT GCCGTCCCGG
GGCAGCACGA CCTCTTCGAC TGCGCGCCGC TCCCCGCCCG CGACTTCCAA CGGCAGGGCC

FIG. 43B

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      1210       1220       1230       1240       1250       1260
TACTGTCGCG CATCGCCAAT TTCGACGACC TCGATCCGCT CGCCGCCGAA CCGGAGATTG
ATGACAGCGC GTAGCGGTTA AAGCTGCTGG AGCTAGGCGA GCGGCGGCTT GGCCTCTAAC

      1270       1280       1290       1300       1310       1320
ATCTCGTCTT CGTGCGGCCT GGCAGTCCCA TTCCGGTCGA CGCTGGCCTC GTCGTCATTC
TAGAGCAGAA GCACGCCGGA CCGTCAGGGT AAGGCCAGCT GCGACCGGAG CAGCAGTAAG

      1330       1340       1350       1360       1370       1380
CCGGGTCGAA ATCGACCATC GGCGACCTCA TCGATTTCCG TGCGCAAGGG TGGGACCGTG
GGCCCAGCTT TAGCTGGTAG CCGCTGGAGT AGCTAAAGGC ACGCGTTCCC ACCCTGGCAC

      1390       1400       1410       1420       1430       1440
ACCTCGAACG TCATGTGCGC CGGGGCGGCC GGGTCATCGG CATCTGCGGC GGCTACCAGA
TGGAGCTTGC AGTACACGCG GCCCCGCCGG CCCAGTAGCC GTAGACGCCG CCGATGGTCT

      1450       1460       1470       1480       1490       1500
TGCTCGGCCG GCGCGTCACC GATCCGCTCG GCATCGAGGG CGGCGAACGT GCGGTCGAGG
ACGAGCCGGC CGCGCAGTGG CTAGGCGAGC CGTAGCTCCC GCCGCTTGCA CGCCAGCTCC

      1510       1520       1530       1540       1550       1560
GCCTCGGGCT GCTCGAGGTC GAGACCGAGA TGGCGCCGGA AAAGACGGTG CGCAACAGCC
CGGAGCCCGA CGAGCTCCAG CTCTGGCTCT ACCGCGGCCT TTTCTGCCAC GCGTTGTCGG

      1570       1580       1590       1600       1610       1620
GCGCCTGGTC GCTGGAGCAT GATGTGGTGC TCGAAGGCTA CGAAATCCAT CTTGGCAAGA
CGCGGACCAG CGACCTCGTA CTACACCACG AGCTTCCGAT GCTTTAGGTA GAACCGTTCT

      1630       1640       1650       1660       1670       1680
CGCAAGGTGC GGACTGTGGC CGGCCGTCGG TGCGCATCGA CAATCGCGCC GACGGCGCCC
GCGTTCCACG CCTGACACCG GCCGGCAGCC ACGCGTAGCT GTTAGCGCGG CTGCCGCGGG

      1690       1700       1710       1720       1730       1740
TTTCGGCCGA TGGCCGCGTG ATGGGCACCT ACCTGCATGG GCTCTTCACC AGCGACGCCT
AAAGCCGGCT ACCGGCGCAC TACCCGTGGA TGGACGTACC CGAGAAGTGG TCGCTGCGGA

      1750       1760       1770       1780       1790       1800
ATCGCGGCGC GCTGCTCAAG AGTTTCGGCA TCGAAGGCGG CGCCAACAAC TACCGCCAAT
TAGCGCCGCG CGACGAGTTC TCAAAGCCGT AGCTTCCGCC GCGGTTGTTG ATGGCGGTTA
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FIG. 43C

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      1810       1820       1830       1840       1850       1860
CGGTCGATGC GGCGCTCGAC GATGTCGCGA ACGAACTGGA GGCTGTGCTC GATCGTCGCT
GCCAGCTACG CCGCGAGCTG CTACAGCGCT TGCTTGACCT CCGACACGAG CTAGCAGCGA

      1870       1880       1890       1900       1910       1920
GGCTGGACGA GTTGCTCAGG CACTAGGGAC GCGGCAACGG TCAGCCAGCA GGTCCGGTAC
CCGACCTGCT CAACGAGTCC GTGATCCCTG CGCCGTTGCC AGTCGGTCGT CCAGGCCATG

      1930       1940       1950       1960       1970       1980
GTCGGGCCCA ACAGGAGCAA CGAGCTTATC CGACGGAACT ACGCTGCGAC ATCGTGCTCC
CAGCCCGGGT TGTCCTCGTT GCTCGAATAG GCTGCCTTGA TGCGACGCTG TAGCACGAGG

      1990       2000       2010       2020       2030       2040
TCGCTTGCGG CTTCCCAGAC TTCCCGCGCG GCATCCAGGT TCATCAGGGC AATCCCCAGG
AGCGAACGCC GAAGGGTCTG AAGGGCGCGC CGTAGGTCCA AGTAGTCCCG TTAGGGGTCC

      2050       2060       2070       2080       2090       2100
CCGACGATCA GGTCCGGCCA GGCCGACTGC CACAGATAGG CTGTCGCCAG ACCCGCGGCG
GGCTGCTAGT CCAGGCCGGT CCGGCTGACG GTGTCTATCC GACAGCGGTC TGGGCGCCGC

      2110       2120       2130       2140       2150       2160
ATGATGGCCA CATTGGCGAA GGCATCGTTG CGGGCCGAGA GAAATGCTGC CCGCGTGAGC
TACTACCGGT GTAACCGCTT CCGTAGCAAC GCCCGGCTCT CTTTACGACG GGCGCACTCG

      2170       2180       2190       2200       2210       2220
GTGCCGCTCG TGTGACGGTA GGCGACGAGC AGATAGGCGC AGAAGAGGTT GACCACCAGC
CACGGCGAGC ACACTGCCAT CCGCTGCTCG TCTATCCGCG TCTTCTCCAA CTGGTGGTCG

      2230       2240       2250       2260       2270       2280
GCCCCAAGTC CGGTCAGGGA CAGGGCAAAG GGCTCTGGCG GGACCGGATC CATGAACTTC
CGGGGTTCAG GCCAGTCCCT GTCCCGTTTC CCGAGACCGC CCTGGCCTAG GTACTTGAAG

      2290       2300       2310       2320       2330       2340
GCCCAGGCCG TCCAAAGGAA GGCCAGCGCC GGTACCAGTA GAATGAACGC CATCGCCATG
CGGGTCCGGC AGGTTTCCTT CCGGTCGCGG CCATGGTCAT CTTACTTGCG GTAGCGGTAC

      2350       2360       2370       2380       2390       2400
CCGACCCGCG CGCGGGTTCG CGCCGTCCAG GCCAGAGCAA AGAAAATCAG CATGTTGACG
GGCTGGGCGC GCGCCCAAGC GCGGCAGGTC CGGTCTCGTT TCTTTTAGTC GTACAACTGG
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FIG. 43D

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      2410       2420       2430       2440       2450       2460
GAGGCGTCTT CGAGGAAGTC GACGCTGTCG GCCATGAGGG ACACCGAGCC GATCGAAAGC
CTCCGCAGAA GCTCCTTCAG CTGCGACAGC CGGTACTCCC TGTGGCTCGG CTAGCTTTCG

      2470       2480       2490       2500       2510       2520
GCGACAAGGA GTTCGACCCC GAAATAGCCA AGGTTCAACA GGGAGACGAT GAGGACGACG
CGCTGTTCCT CAAGCTGGGG CTTTATCGGT TCCAAGTTGT CCCTCTGCTA CTCCTGCTGC

      2530       2540       2550       2560       2570       2580
CGGCGCAGGT CGGTATCCAC TCGAAAGGTT CCCTTTCTGG CGAGATTCGC CCTCGGCACT
GCCGCGTCCA GCCATAGGTG AGCTTTCCAA GGGAAAGACC GCTCTAAGCG GGAGCCGTGA

      2590       2600       2610       2620       2630       2640
TTTTTTGGCG AGATTCGCCC TCGGCACTTT GGCACAGGTG TTAGCAGCAG TTTGCTATCC
AAAAAACCGC TCTAAGCGGG AGCCGTGAAA CCGTGTCCAC AATCGTCGTC AAACGATAGG

      2650       2660       2670       2680       2690       2700
ATAGCACTAG GTTTCGACAT CGGTTCCGTT CACACTGCCG TCGTGCCTGA CGCCCGACAA
TATCGTGATC CAAAGCTGTA GCCAAGGCAA GTGTGACGGC AGCACGGACT GCGGGCTGTT

      2710       2720       2730       2740       2750       2760
ATCGTCGCGT GGCGCAACTC GGCCGGGGAG GCGTCGCATG CGTCGATTGA CTTTGGGCTG
TAGCAGCGCA CCGCGTTGAG CCGGCCCCTC CGCAGCGTAC GCAGCTAACT GAAACCCGAC

      2770       2780       2790       2800       2810       2820
CCCGCTTCCT AATCATCAGG TGTTGGATGG TTCCCCCTTG TCGTGGCGAT CTGGGGGAAT
GGGCGAAGGA TTAGTAGTCC ACAACCTACC AAGGGGGAAC AGCACCGCTA GACCCCCTTA

      2830       2840       2850       2860       2870       2880
AATTGGGAAT GTGACGGATG GACCCAAATC GGGCATCCTT ATCGCAGCCG ACCCCGCGAC
TTAACCCTTA CACTGCCTAC CTGGGTTTAG CCCGTAGGAA TAGCGTCGGC TGGGGCGCTG

      2890       2900       2910       2920       2930       2940
TGTAGAACGG TCAGGGTTCG CCATCGGGAT TGGTGCCGGG CTGTCGGCCG GTTGCATGGG
ACATCTTGCC AGTCCCAAGC GGTAGCCCTA ACCACGGCCC GACAGCCGGC CAACGTACCC

      2950       2960       2970       2980       2990       3000
CAATCGGGGC AGGTCGGGGA TCAAGCCGGA AAAGCCACTG GCGTGGCATC GTGATCAGCC
GTTAGCCCCG TCCAGCCCCT AGTTCGGCCT TTTCGGTGAC CGCACCGTAG CACTAGTCGG
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FIG. 43E

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      3010       3020       3030       3040       3050       3060
GGGTTTGGAC GCCTCTTCTT CTACGAATCG TCCGCCTTTC ACGATGTCCC TCACAGCGCC
CCCAAACCTG CGGAGAAGAA GATGCTTAGC AGGCGGAAAG TGCTACAGGG AGTGTCGCGG

      3070       3080       3090       3100       3110       3120
CATGCGTCGG AGACGACGCG CAAAGGTTCG CTGTGGCACC GGAAAGACGC CGGGAAGGTG
GTACGCAGCC TCTGCTGCGC GTTTCCAAGC GACACCGTGG CCTTTCTGCG GCCCTTCCAC

      3130       3140       3150       3160       3170       3180
AGGCGGGCCG CTCGGGCCCT GACATCGGAA CCTTGCCGTT TAAGGGCGAG GCGATGTTCG
TCCGCCCGGC GAGCCCGGGA CTGTAGCCTT GGAACGGCAA ATTCCCGCTC CGCTACAAGC

      3190       3200       3210       3220       3230       3240
GCCCGTGACG CCGTGAGCCA GGAGACCTGC CATCCGGCAT GGGCATTCCG CCCGAGGGGA
CGGGCACTGC GGCACTCGGT CCTCTGGACG GTAGGCCGTA CCCGTAAGGC GGGCTCCCCT

      3250       3260       3270       3280       3290       3300
CTTTTGTCTC CAACGCCATC ACGGAGGTTG TTTTGGCTCG CAGATGTTTT CAAGAACGCG
GAAAACAGAG GTTGCGGTAG TGCCTCCAAC AAAACCGAGC GTGTACAAAA GTTCTTGCGC

      3310       3320       3330       3340       3350       3360
CCCGTGGCGC GTCCGATGGC TTTTGCCACC GACGGCTGAT TTGGGAATGT TGAGGCAGCC
GGGCACCGCG CAGGCTACCG AAAACGGTGG CTGCCGACTA AACCCTTACA ACTCCGTCGG

      3370       3380       3390       3400       3410       3420
ACGATGAGCA GTCTCAGCGC CGGGCCCGTG CTGGTCCTTG GCGGCGCCCG TTCCGGCAAG
TGCTACTCGT CAGAGTCGCG GCCCGGGCAC GACCAGGAAC CGCCGCGGGC AAGGCCGTTC

      3430       3440       3450       3460       3470       3480
TCCAGCTTTT CCGAGAGGCT CGTCGAAGCG TCCGGCTTCA CCATGCATTA TGTCGCCACG
AGGTCGAAAA GGCTCTCCGA GCAGCTTCGC AGGCCGAAGT GGTACGTAAT ACAGCGGTGC

      3490       3500       3510       3520       3530       3540
GGCCGCGCCT GGGACGACGA AATGCGCGAG CGCATCGACC ATCACCGGAC GCGCCGCGGC
CCGGCGCGGA CCCTGCTGCT TTACGCGCTC GCGTAGCTGG TAGTGGCCTG CGCGGCGCCG

      3550       3560       3570       3580       3590       3600
GAGGGCTGGA CGACGCATGA GGAGCCGCTC GATCTCGTCG GCATCCTCAG ACGCATCGAT
CTCCCGACCT GCTGCGTACT CCTCGGCGAG CTAGAGCAGC CGTAGGAGTC TGCGTAGCTA
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FIG. 43F

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      3610       3620       3630       3640       3650       3660
GATCCCAGCC ATGTGGTCCT GATCGACTGC CTGACGCTAT GGGTCACCAA TCTCATGCTG
CTAGGGTCGG TACACCAGGA CTAGCTGACG GACTGCGATA CCCAGTGGTT AGAGTACGAC

      3670       3680       3690       3700       3710       3720
GAAGAGCGCG ACATGACGGC GGAGTTCGCC GCCCTTGTTG CGTATCTGCC CGAGGCGCGG
CTTCTCGCGC TGTACTGCCG CCTCAAGCGG CGGGAACAAC GCATAGACGG GCTCCGCGCC

      3730       3740       3750       3760       3770       3780
GCGCGCCTCG TCTTTGTTTC CAATGAGGTC GGCCTCGGCA TCGTGCCCGA GAACCGCATG
CGCGCGGAGC AGAAACAAAG GTTACTCCAG CCGGAGCCGT AGCACGGGCT CTTGGCGTAC

      3790       3800       3810       3820       3830       3840
GCCCGCGAGT TTCGCGACCA TGCCGGCCGG CTTCACCAGA TCGTTGCGGA GAAATCCGCT
CGGGCGCTCA AAGCGCTGGT ACGGCCGGCC GAAGTGGTCT AGCAACGCCT CTTTAGGCGA

      3850       3860       3870       3880       3890       3900
GAAGTTTACT TTGTCGCGGC CGGTTTGCCG CTGAAAATGA AGGGTTGATC CATGACCACT
CTTCAAATGA AACAGCGCCG GCCAAACGGC GACTTTTACT TCCCAACTAG GTACTGGTGA

      3910       3920       3930       3940       3950       3960
GCGAGAGCCA ACCAGGGCAA GATCCCGGCG ACCGTCATCA CCGGCTTCCT CGGCGCCGGC
CGCTCTCGGT TGGTCCCGTT CTAGGGCCGC TGGCAGTAGT GGCCGAAGGA GCCGCGGCCG

      3970       3980       3990       4000       4010       4020
AAGACGACGA TGATCCGCAA CCTGCTGCAG AACGCCGACG GCAAGCGCAT CGGCCTGATC
TTCTGCTGCT ACTAGGCGTT GGACGACGTC TTGCGGCTGC CGTTCGCGTA GCCGGACTAG

      4030       4040       4050       4060       4070       4080
ATCAACGAGT TCGGCGATCT TGGCGTCGAC GGCGATGTCT TGAAGGGCTG CGGTGCCGAC
TAGTTGCTCA AGCCGCTAGA ACCGCAGCTG CCGCTACAGA ACTTCCCGAC GCCACGGCTC

      4090       4100       4110       4120       4130       4140
GCCTGCACCG AGGACGACAT CATCGAGCTC ACCAATGGCT GCATCTGCTG CACCGTGGCT
CGGACGTGGC TCCTGCTGTA GTAGCTCGAG TGGTTACCGA CGTAGACGAC GTGGCACCGA

      4150       4160       4170       4180       4190       4200
GACGATTTCA TCCCGACCAT GACGAAGCTG CTCGAGCGTG AAAACCGTCC TGACCACATC
CTGCTAAAGT AGGGCTGGTA CTGCTTCGAC GAGCTCGCAC TTTTGGCAGG ACTGGTGTAG
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FIG. 43G

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      4210       4220       4230       4240       4250       4260
ATCATCGAAA CCTCGGGCCT TGCCCTGCCG CAGCCGCTGA TCGCCGCTTT CAACTGGCCG
TAGTAGCTTT GGAGCCCGGA ACGGGACGGC GTCGGCGACT AGCGGCGAAA GTTGACCGGC

      4270       4280       4290       4300       4310       4320
GATATCCGCA GCGAAGTGAC CGTCGATGGC GTCGTCACCG TGGTCGACAG CGCCGCCGTT
CTATAGGCGT CGCTTCACTG GCAGCTACCG CAGCAGTGGC ACCAGCTGTC GCGGCGGCAA

      4330       4340       4350       4360       4370       4380
GCCGCTGGCC GCTTTGCCGA CGACCACGAC AAGGTCGATG CGCTGCGCGT CGAGGACGAC
CGGCGACCGG CGAAACGGCT GCTGGTGCTG TTCCAGCTAC GCGACGCGCA GCTCCTGCTG

      4390       4400       4410       4420       4430       4440
AATCTCGATC ACGAAAGCCC GATCGAGGAG CTGTTCGAGG ATCAACTGAC GGCTGCCGAT
TTAGAGCTAG TGCTTTCGGG CTAGCTCCTC GACAAGCTCC TAGTTGACTG CCGACGGCTA

      4450       4460       4470       4480       4490       4500
CTCATCGTTC TCAACAAGAC CGATCTGATC GATGCCTCCG GCCTCAAGGC CGTGCGCGAC
GAGTAGCAAG AGTTGTTCTG GCTAGACTAG CTACGGAGGC CGGAGTTCCG GCACGCGCTG

      4510       4520       4530       4540       4550       4560
GAGGTGTCTT CGCGCACCAG CCGCAAGCCC ACGATGATCG AGGCGAAAAA CGGCGAAGTC
CTCCACAGAA GCGCGTGGTC GGCGTTCGGG TGCTACTAGC TCCGCTTTTT GCCGCTTCAG

      4570       4580       4590       4600       4610       4620
GCCGCTGCCA TCCTGCTTGG CCTCGGTGTC GGCACGGAAA GCGATATCGC CAACCGCAAG
CGGCGACGGT AGGACGAACC GGAGCCACAG CCGTGCCTTT CGCTATAGCG GTTGGCGTTC

      4630       4640       4650       4660       4670       4680
TCGCATCACG AGATGGAGCA CGAGGCAGGT GAGGAGCACG ATCACGACGA GTTCGACAGC
AGCGTAGTGC TCTACCTCGT GCTCCGTCCA CTCCTCGTGC TAGTGCTGCT CAAGCTGTCG

      4690       4700       4710       4720       4730       4740
TTCGTCGTCG AGCTCGGTTC GATCGCCGAT CCGGCCGCCT TCATCGATCG CCTGAAGGGC
AAGCAGCAGC TCGAGCCAAG CTAGCGGCTA GGCCGGCGGA AGTAGCTAGC GGACTTCCCG

      4750       4760       4770       4780       4790       4800
GTAATCGCGG AGCACGACGT TCTGCGCCTC AAGGGTTTTG CAGACGTGCC CGGCAAGCCG
CATTAGCGCC TCGTGCTGCA AGACGCGGAG TTCCCAAAAC GTCTGCACGG GCCGTTCGGC
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FIG. 43H

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      4810       4820       4830       4840       4850       4860
ATGCGCCTCC TGATCCAGGC GGTCGGCGCC CGCATCGACC AATATTACGA CCGCGCCTGG
TACGCGGAGG ACTAGGTCCG CCAGCCGCGG GCGTAGCTGG TTATAATGCT GGCGCGGACC

      4870       4880       4890       4900       4910       4920
GGCGCTGGCG AAAAGCGCGG TACGCGCCTC GTCGTCATCG GCCTGCACGA CATGGACGAG
CCGCGACCGC TTTTCGCGCC ATGCGCGGAG CAGCAGTAGC CGGACGTGCT GTACCTGCTC

      4930       4940       4950       4960       4970       4980
GCGGCGGTGC GCGCCGCGAT CACCGCGCTC GTGTAGATCG TTCTTTGAAT GAAATGATCT
CGCCGCCACG CGCGGCGCTA GTGGCGCGAG CACATCTAGC AAGAAACTTA CTTTACTAGA

      4990       5000       5010       5020       5030       5040
AACGCATTGA AATGATGCAG TTCCGGATGG AGAACGCTTT TAGCGTTTTC GTTCGGAATT
TTGCGTAACT TTACTACGTC AAGGCCTACC TCTTGCGAAA ATCGCAAAAG CAAGCCTTAA

      5050       5060       5070       5080       5090       5100
GCCCCAACGG ACAAGACGAA TGCATCTGCT TCTCGCCCAG AAAGGAACGA TCGCCGACGG
CGGGGTTGCC TGTTCTGCTT ACGTAGACGA AGAGCGGGTC TTTCCTTGCT AGCGGCTGCC

      5110       5120       5130       5140       5150       5160
CAACGAGGCG ATCGACCTTG GGCAAACGCC GGCCGATATC CTTTTCCTAT CGGCCGCCGA
GTTGCTCCGC TAGCTGGAAC CCGTTTGCGG CCGGCTATAG GAAAAGGATA GCCGGCGGCT

      5170       5180       5190       5200       5210       5220
CACCGAGCTC TCCTCGATCG CCGCGGCTCA CGGCCGACGC GACGGAGGCT TGAGCCTGCG
GTGGCTCGAG AGGAGCTAGC GGCGCCGAGT GCCGGCTGCG CTGCCTCCGA ACTCGGACGC

      5230       5240       5250       5260       5270       5280
CATCGCCAGC CTGATGAGCC TGATGCACCC GATGTCGGTC GACACTTACG TCGAGCGCAC
GTAGCGGTCG GACTACTCGG ACTACGTGGG CTACAGCCAG CTGTGAATGC AGCTCGCGTG

      5290       5300       5310       5320       5330       5340
GGCGCGTCAC GCCAAGCTGA TCGTCGTCCG GCCGCTCGGT GGCGCCAGCT ATTTCCGTTA
CCGCGCAGTG CGGTTCGACT AGCAGCAGGC CGGCGAGCCA CCGCGGTCGA TAAAGGCAAT

      5350       5360       5370       5380       5390       5400
TCTGCTGGAA GCCCTGCATG CGGCTGCCGT CACCCATCGT TTCGAGATCG CGGTTCTGCC
AGACGACCTT CGGGACGTAC GCCGACGGCA GTGGGTAGCA AAGCTCTAGC GCCAAGACGG
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FIG. 43I

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      5410       5420       5430       5440       5450       5460
GGGTGACGAC AAGCCGGATC CGGGGCTGGA GCCTTTCTCC ACCGTCGCAG CCGACGACCG
CCCACTGCTG TTCGGCCTAG GCCCCGACCT CGGAAAGAGG TGGCAGCGTC GGCTGCTGGC

      5470       5480       5490       5500       5510       5520
CCAGCGCCTT TGGGCTTACT TCACCGAAGG CGGCTCGGAC AATGCCGGGC TGTTTCTCGA
GGTCGCGGAA ACCCGAATGA AGTGGCTTCC GCCGAGCCTG TTACGGCCCG ACAAAGAGCT

      5530       5540       5550       5560       5570       5580
CTATGCGGCC GCACTGGTCA CAGGTGCGGA GAAGCCGCAG CCGGCAAAGC CCCTGTTGAA
GATACGCCGG CGTGACCAGT GTCCACGCCT CTTCGGCGTC GGCCGTTTCG GGGACAACTT

      5590       5600       5610       5620       5630       5640
GGCCGGCATC TGGTGGCCGG GTGCTGGTGT GATCGGCGTC AGCGAATGGC AGTCCCTTGT
CCGGCCGTAG ACCACCGGCC CACGACCACA CTAGCCGCAG TCGCTTACCG TCAGGGAACA

      5650       5660       5670       5680       5690       5700
TCAGGGACGG ATGGTAGCGA GGGAGGGATT CGAACCCCCG ACGGTCGGGA TCTGCTTTTA
AGTCCCTGCC TACCATCGCT CCCTCCCTAA GCTTGGGGGC TGCCAGCCCT AGACGAAAAT

      5710       5720       5730       5740       5750       5760
CCGCGCGCTC GTGCAGAGTG GCGAGACACG GCCTGTGGAG GCGCTGATCG ATGCGCTGGA
GGCGCGCGAG CACGTCTCAC CGCTCTGTGC CGGACACCTC CGCGACTAGC TACGCGACCT

      5770       5780       5790       5800       5810       5820
GGCTGAAGGT GTGCGGGCAC TGCCGGTGTT TGTCTCAAGC CTCAAGGATG CCGTTTCCGT
CCGACTTCCA CACGCCCGTG ACGGCCACAA ACAGAGTTCG GAGTTCCTAC GGCAAAGGCA

      5830       5840       5850       5860       5870       5880
CGGCACGCTG CAGGCGATTT TTTCCGAGGC CGCACCCGAC GTGGTGATGA ACGCCACTGG
GCCGTGCGAC GTCCGCTAAA AAAGGCTCCG GCGTGGGCTG CACCACTACT TGCGGTGACC

      5890       5900       5910       5920       5930       5940
CTTTGCGGTC TCGTCGCCCG GTGCCGACCG TCAGCCGACG GTGCTGGAAT CGACCGGTGC
GAAACGCCAG AGCAGCGGGC CACGGCTGGC AGTCGGCTGC CACGACCTTA GCTGGCCACG

      5950       5960       5970       5980       5990       6000
GCCGGTGCTG CAGGTGATTT TCTCCGGCTC GTCGCGGGCG CAATGGGAAA CGTCGCCGCA
CGGCCACGAC GTCCACTAAA AGAGGCCGAG CAGCGCCCGC GTTACCCTTT GCAGCGGCGT
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FIG. 43J

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      6010       6020       6030       6040       6050       6060
GGGGCTGATG GCGCGCGACC TCGCCATGAA CGTGGCACTC CCCGAAGTCG ATGGCCGCAT
CCCCGACTAC CGCGCGCTGG AGCGGTACTT GCACCGTGAG GGGCTTCAGC TACCGGCGTA

      6070       6080       6090       6100       6110       6120
CCTTGCGCGC GCCGTCTCCT TCAAGGCGGC GTCGATCTAT GACGCCAAGG TGGAGGCCAA
GGAACGCGCG CGGCAGAGGA AGTTCCGCCG CAGCTAGATA CTGCGGTTCC ACCTCCGGTT

      6130       6140       6150       6160       6170       6180
TATCGTCGGC CATGAGCCGC TCGAAGGCCG GGTGCGCTTT GCCGCTGATC TTGCCGTCAA
ATAGCAGCCG GTACTCGGCG AGCTTCCGGC CCACGCGAAA CGGCGACTAG AACGGCAGTT

      6190       6200       6210       6220       6230       6240
CTGGGCGAAC GTGCGCCGGG CAGAGCCCGC CGAGCGCCGT ATTGCCATCG TCATGGCCAA
GACCCGCTTG CACGCGGCCC GTCTCGGGCG GCTCGCGGCA TAACGGTAGC AGTACCGGTT

      6250       6260       6270       6280       6290       6300
CTATCCGAAC CGCGACGGTC GCCTCGGCAA CGGTGTCGGG CTCGACACGC CGGCCGGTAC
GATAGGCTTG GCGCTGCCAG CGGAGCCGTT GCCACAGCCC GAGCTGTGCG GCCGGCCATG

      6310       6320       6330       6340       6350       6360
CGTCGAGGTG CTTAGCGCCA TGGCGCGGGA AGGCTATGCG GTCGGTGAGG TTCCCGCCGA
GCAGCTCCAC GAATCGCGGT ACCGCGCCCT TCCGATACGC CAGCCACTCC AAGGGCGGCT

      6370       6380       6390       6400       6410       6420
TGGCGACGCG CTGATCCGCT TTCTGATGGC CGGGCCGACC AATGCGGCGA GCCATGACCG
ACCGCTGCGC GACTAGGCGA AAGACTACCG GCCCGGCTGG TTACGCCGCT CGGTACTGGC

      6430       6440       6450       6460       6470       6480
TGAAATCCGC GAGCGTATTT CGCTGAACGA TTACAAAACG TTCTTCGATT CGCTTCCGAA
ACTTTAGGCG CTCGCATAAA GCGACTTGCT AATGTTTTGC AAGAAGCTAA GCGAAGGCTT

      6490       6500       6510       6520       6530       6540
ACAGATAAAG GATGAAGTTG CCGGTCGCTG GGGCGTGCCG GAGGCCGATC CCTTTTTCCT
TGTCTATTTC CTACTTCAAC GGCCAGCGAC CCCGCACGGC CTCCGGCTAG GGAAAAAGGA

      6550       6560       6570       6580       6590       6600
CGATGGCGCC TTCGCGCTGC CGCTCGCCCG CTTCGGCGAG GTGATCGTCG GCATCCAACC
GCTACCGCGG AAGCGCGACG GCGAGCGGGC GAAGCCGCTC CACTAGCAGC CGTAGGTTGG
```

FIG. 43K

```
      6610       6620       6630       6640       6650       6660
GGCGCGCGGC TACAACATCG ATCCGAAGGA AAGCTACCAT TCCCCGGACC TCGTGCCGCC
CCGCGCGCCG ATGTTGTAGC TAGGCTTCCT TTCGATGGTA AGGGGCCTGG AGCACGGCGG

      6670       6680       6690       6700       6710       6720
GCATGGCTAT CTCGCCTTCT ACGCCTTCCT GCGCCAGCAG TTCGGAGCGC AGGCGATCGT
CGTACCGATA GAGCGGAAGA TGCGGAAGGA CGCGGTCGTC AAGCCTCGCG TCCGCTAGCA

      6730       6740       6750       6760       6770       6780
CCACATGGGC AAGCACGGCA ATCTCGAATG GCTGCCGGGC AAGGCGCTGG CGCTGTCGGA
GGTGTACCCG TTCGTGCCGT TAGAGCTTAC CGACGGCCCG TTCCGCGACC GCGACAGCCT

      6790       6800       6810       6820       6830       6840
AACCTGCTAT CCCGAAGCGA TCTTCGGGCC GCTGCCGCAC ATCTATCCCT TCATCGTCAA
TTGGACGATA GGGCTTCGCT AGAAGCCCGG CGACGGCGTG TAGATAGGGA AGTAGCAGTT

      6850       6860       6870       6880       6890       6900
CGATCCGGGC GAAGGTACGC AGGCCAAGCG CCGCACCAGC GCCGTCATCA TCGACCACCT
GCTAGGCCCG CTTCCATGCG TCCGGTTCGC GGCGTGGTCG CGGCAGTAGT AGCTGGTGGA

      6910       6920       6930       6940       6950       6960
GACCCCGCCC TTGACGCGCG CCGAATCCTA CGGCCCGCTC AAGGATCTGG AAGCGCTCGT
CTGGGGCGGG AACTGCGCGC GGCTTAGGAT GCCGGGCGAG TTCCTAGACC TTCGCGAGCA

      6970       6980       6990       7000       7010       7020
CGACGAATAT TACGACGCCG CCGGCGGTGA TCCGCGCCGC CTCAGGCTGC TCAGCCGCCA
GCTGCTTATA ATGCTGCGGC GGCCGCCACT AGGCGCGGCG GAGTCCGACG AGTCGGCGGT

      7030       7040       7050       7060       7070       7080
GATCCTCGAT CTCGTGCGCG ACATCGGCCT CGACAGCGAC GCAGGCATCG ACAGGGGCGA
CTAGGAGCTA GAGCACGCGC TGTAGCCGGA GCTGTCGCTG CGTCCGTAGC TGTCCCCGCT

      7090       7100       7110       7120       7130       7140
CAGCGACGAC AAGGCGCTGG AAAAGCTCGA CGCCTATCTC TGCGACCTCA AGGAAATGCA
GTCGCTGCTG TTCCGCGACC TTTTCGAGCT GCGGATAGAG ACGCTGGAGT TCCTTTACGT

      7150       7160       7170       7180       7190       7200
GATCCGCGAC GGCCTGCACA TCTTCGGCGT TGCGCCGGAA GGGCGGTTGT TGACGGACCT
CTAGGCGCTG CCGGACGTGT AGCCGCCGCA ACGCGGCCTT CCCGCCAACA ACTGCCTGGA
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FIG. 43L

7210	7220	7230	7240	7250	7260
CACCGTAGCG	CTGGCGCGCG	TGCCCCGAGG	TCTCGGCGAG	GGCGGCGACC	AGAGCCTGCA
GTGGCATCGC	GACCGCGCGC	ACGGGGCTCC	AGAGCCGCTC	CCGCCGCTGG	TCTCGGACGT
7270	7280	7290	7300	7310	7320
GCGGGCGATC	GCAGCGGATG	CGGGGCTGCG	TGGGTTTGCT	ATTCCCACCT	CGGCGGGGGG
CGCCCGCTAG	CGTCGCCTAC	GCCCCGACGC	ACCCAAACGA	TAAGGGTGGA	GCCGCCCCCC
7330	7340	7350	7360	7370	7380
CAACCCCGCA	CGCGACGCCC	AACCCTTCGA	CCCGCTCGAC	TGCGTCATGT	CCGACACCTG
GTTGGGGCGT	GCGCTGCGGG	TTGGGAAGCT	GGGCGAGCTG	ACGCAGTACA	GGCTGTGGAC
7390	7400	7410	7420	7430	7440
GACAGGCCCG	AAACCGTCCA	TCCTCGCTGA	CCTCTCGGAC	GCCCCCTGGC	GCACCGCCGG
CTGTCCGGGC	TTTGGCAGGT	AGGAGCGACT	GGAGAGCCTG	CGGGGGACCG	CGTGGCGGCC
7450	7460	7470	7480	7490	7500
CGATACGGTC	GAGCGCATCG	AGTTGCTTGC	CGCAAATCTC	GTGTCGGGTG	AACTGGCTTG
GCTATGCCAG	CTCGCGTAGC	TCAACGAACG	GCGTTTAGAG	CACAGCCCAC	TTGACCGAAC
7510	7520	7530	7540	7550	7560
CCCGGACCAC	TGGGCCAACA	CCCGCGCCGT	GCTCGGCGAA	ATCGAAACGC	GCCTGAAGCC
GGGCCTGGTG	ACCCGGTTGT	GGGCGCGGCA	CGAGCCGCTT	TAGCTTTGCG	CGGACTTCGG
7570	7580	7590	7600	7610	7620
GTCGATTTCA	AACTCGGGTG	CCGCCGAGAT	GACCGGCTTC	CTCACCGGTC	TCAGCGGCCG
CAGCTAAAGT	TTGAGCCCAC	GGCGGCTCTA	CTGGCCGAAG	GAGTGGCCAG	AGTCGCCGGC
7630	7640	7650	7660	7670	7680
CTTCGTCGCC	CCCGGTCCAT	CGGGCGCGCC	GACGCGCGGC	CGGCCGGATG	TGTTGCCGAC
GAAGCAGCGG	GGGCCAGGTA	GCCCGCGCGG	CTGCGCGCCG	GCCGGCCTAC	ACAACGGCTG
7690	7700	7710	7720	7730	7740
GGGGCGCAAT	TTCTACTCGG	TCGACAGCCG	CGCCGTGCCG	ACGCCGGCGG	CTTACGAGCT
CCCCGCGTTA	AAGATGAGCC	AGCTGTCGGC	GCGGCACGGC	TGCGGCCGCC	GAATGCTCGA
7750	7760	7770	7780	7790	7800
TGGCAAGAAA	TCGGCCGAGC	TTCTGATCCG	CCGCTACCTG	CAGGACCATG	GCGAATGGCC
ACCGTTCTTT	AGCCGGCTCG	AAGACTAGGC	GGCGATGGAC	GTCCTGGTAC	CGCTTACCGG

FIG. 43M

```
      7810       7820       7830       7840       7850       7860
GTCCTCCTTT GGCCTGACCG CCTGGGGCAC GGCGAACATG CGCACCGGCG GCGACGACAT
CAGGAGGAAA CCGGACTGGC GGACCCCGTG CCGCTTGTAC GCGTGGCCGC CGCTGCTGTA

      7870       7880       7890       7900       7910       7920
CGCCCAGGCC CTGGCGCTGA TCGGCGCCAA GCCCACCTGG GACATGGTCT CTCGCCGGGT
GCGGGTCCGG GACCGCGACT AGCCGCGGTT CGGGTGGACC CTGTACCAGA GAGCGGCCCA

      7930       7940       7950       7960       7970       7980
GATGGGCTAC GAGATCGTGC CGCTCGCAGT CCTCGGCCGC CCACGCGTCG ACGTGACCTT
CTACCCGATG CTCTAGCACG GCGAGCGTCA GGAGCCGGCG GGTGCGCAGC TGCACTGGAA

      7990       8000       8010       8020       8030       8040
GCGCATTTCC GGCTTCTTCC GCGATGCCTT CCCGGACCAG ATCGCGCTCT TCGACAAGGC
CGCGTAAAGG CCGAAGAAGG CGCTACGGAA GGGCCTGGTC TAGCGCGAGA AGCTGTTCCG

      8050       8060       8070       8080       8090       8100
GATCCGCGCC GTCGCGCTGG AGGAAGACGA TGCCGACAAC ATGATCGCCG CACGCATGCG
CTAGGCGCGG CAGCGCGACC TCCTTCTGCT ACGGCTGTTG TACTAGCGGC GTGCGTACGC

      8110       8120       8130       8140       8150       8160
GGCGGAAAGC CGGCGGCTGG AGGCCGAAGG CGTGGAAGCC GCCGAGGCCG CGCGTCGCGC
CCGCCTTTCG GCCGCCGACC TCCGGCTTCC GCACCTTCGG CGGCTCCGGC GCGCAGCGCG

      8170       8180       8190       8200       8210       8220
CTCCTACCGC GTCTTTGGCG CAAAGCCCGG TGCCTATGGC GCCGCCCTGC AGGCGCTGAT
GAGGATGGCG CAGAAACCGC GTTTCGGGCC ACGGATACCG CGGCGGGACG TCCGCGACTA

      8230       8240       8250       8260       8270       8280
CGACGAGAAG GGCTGGGAAA CCAAAGCAGA TCTCGCCGAG GCCTATCTTA CCTGGGGCGC
GCTGCTCTTC CCGACCCTTT GGTTTCGTCT AGAGCGGCTC CGGATAGAAT GGACCCCGCG

      8290       8300       8310       8320       8330       8340
CTATGCCTAT GGCGCCGGCG AGGAGGGCAA GGCCGAGCGC GATCTTTTCG AGGAGCGCCT
GATACGGATA CCGCGGCCGC TCCTCCCGTT CCGGCTCGCG CTAGAAAAGC TCCTCGCGGA

      8350       8360       8370       8380       8390       8400
GCGCACGATA GAGGCGGTGG TGCAGAACCA GGACAACCGC GAGCACGATC TGCTCGACAG
CGCGTGCTAT CTCCGCCACC ACGTCTTGGT CCTGTTGGCG CTCGTGCTAG ACGAGCTGTC
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FIG. 43N

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      8410       8420       8430       8440       8450       8460
CGACGACTAC TACCAGTTCG AAGGCGGCAT GAGCGCTGCC GCCGAACAGC TCGGCGGTCA
GCTGCTGATG ATGGTCAAGC TTCCGCCGTA CTCGCGACGG CGGCTTGTCG AGCCGCCAGT

      8470       8080       8490       8500       8510       8520
CCGTCCGGCG ATCTACCACA ACGACCATTC CCGTCCGGAA AAGCCTGTGA TCCGGTCGCT
GGCAGGCCGC TAGATGGTGT TGCTGGTAAG GGCAGGCCTT TTCGGACACT AGGCCAGCGA

      8530       8540       8550       8560       8570       8580
CGAAGAAGAG ATCGGCCGCG TGGTCCGGGC CCGCGTCGTC AATCCCAAGT GGATCGATGG
GCTTCTTCTC TAGCCGGCAC ACCAGGCCCG GGCGCAGCAG TTAGGGTTCA CCTAGCTACC

      8590       8600       8610       8620       8630       8640
CGTCATGCGC CACGGATACA AGGGCGCCTT CGAGATCGCT GCCACGGTCG ACTACATGTT
GCAGTACGCG GTGCCTATGT TCCCGCGGAA GCTCTAGCGA CGGTGCCAGC TGATGTACAA

      8650       8660       8670       8680       8690       8700
CGCCTTTGCC GCGACCACGG GTGCGGTGCG CGACCATCAT TTCGAGGCCG CTTATCAGGC
GCGGAAACGG CGCTGGTGCC CACGCCACGC GCTGGTAGTA AAGCTCCGGC GAATAGTCCG

      8710       8720       8730       8740       8750       8760
GTTCATTGTC GACGAGCGCG TGGCTGACTT CATGCGCGAC AAGAACCCGG CCGCCTTTGC
CAAGTAACAG CTGCTCGCGC ACCGACTGAA GTACGCGCTG TTCTTGGGCC GGCGGAAACG

      8770       8780       8790       8800       8810       8820
CGAGCTTGCC GAACGCCTGC TTGAAGCAAT CGACCGCAAT CTCTGGACGC CGCGCTCGAA
GCTCGAACGG CTTGCGGACG AACTTCGTTA GCTGGCGTTA GAGACCTGCG GCGCGAGCTT

      8830       8840       8850       8860       8870       8880
TTCGGCGCGG TTTGAACTTG CCGGCATCGG CACGGCAGCA ACCCGGCTTC GTGCCGGCAA
AAGCCGCGCC AAACTTGAAC GGCCGTAGCC GTGCCGTCGT TGGGCCGAAG CACGGCCGTT

      8890       8900       8910       8920       8930       8940
TGAATAGAGC GGTTCCGGGC TGGCGGTTAT CCGTCCGGAA TTGCTTGGAA ACAAAGACCT
ACTTATCTCG CCAAGGCCCG ACCGCCAATA GGCAGGCCTT AACGAACCTT TGTTTCTGGA

      8950       8960       8970       8980       8990       9000
GGTTCCGTTT CGCTGCTCAG TGAAGTGCGA AAAGGAACCG AAGCGGGACG AGGGCGTCTG
CCAAGGCAAA GCGACGAGTC ACTTCACGCT TTTCCTTGGC TTCACCCTGC TCCCGCAGAC
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FIG. 43O

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      9010       9020       9030       9040       9050       9060
CCCATCCCGA ACTTGAGAAC TGAGGGAGTG ATCATGAGCG ACGAGACGAC AGTAGGCGGC
GGGTAGGGCT TGAACTCTTG ACTCCCTCAC TAGTACTCGC TGCTCTGCTG TCATCCGCCG

      9070       9080       9090       9100       9110       9120
GAAGCCCCGG CCGAGAAGGA CGATGCCCGC CACGCCATGA AGATGGCGAA GAAGAAGGCA
CTTCGGGGCC GGCTCTTCCT GCTACGGGCG GTGCGGTACT TCTACCGCTT CTTCTTCCGT

      9130       9140       9150       9160       9170       9180
GCACGCGAAA AGATCATGGC GACGAAGACC GACGAGAAGG GTCTGATCAT CGTCAACACC
CGTGCGCTTT TCTAGTACCG CTGCTTCTGG CTGCTCTTCC CAGACTAGTA GCAGTTGTGG

      9190       9200       9210       9220       9230       9240
GGCAAAGGCA AGGGCAAGTC GACCGCCGGC TTCGGCATGA TCTTCCGCCA TATCGCCCAC
CCGTTTCCGT TCCCGTTCAG CTGGCGGCCG AAGCCGTACT AGAAGGCGGT ATAGCGGGTG

      9250       9260       9270       9280       9290       9300
GGCATGCCCT GCGCCGTCGT GCAGTTCATC AAGGGTGCGA TGGCAACCGG CGAGCGCGAG
CCGTACGGGA CGCGGCAGCA CGTCAAGTAG TTCCCACGCT ACCGTTGGCC GCTCGCGCTC

      9310       9320       9330       9340       9350       9360
TTGATCGAGA AGCATTTCGG CGATGTCTGC CAGTTCTACA CGCTCGGCGA GGGCTTCACC
AACTAGCTCT TCGTAAAGCC GCTACAGACG GTCAAGATGT GCGAGCCGCT CCCGAAGTGG

      9370       9380       9390       9400       9410       9420
TGGGAAACGC AGGATCGCGC CCGCGATGTT GCGATGGCTG AAAAGGCCTG GGAGAAGGCG
ACCCTTTGCG TCCTAGCGCG GGCGCTACAA CGCTACCGAC TTTTCCGGAC CCTCTTCCGC

      9430       9440       9450       9460       9470       9480
AAGGAACTGA TCCGTGACGA GCGCAACTCG ATGGTGCTGC TCGACGAGAT CAACATTGCT
TTCCTTGACT AGGCACTGCT CGCGTTGAGC TACCACGACG AGCTGCTCTA GTTGTAACGA

      9490       9500       9510       9520       9530       9540
CTGCGCTACG ACTACATCGA CGTCGCCGAA GTGGTGCGCT TCCTGAAGGA AGAAAAGCCG
GACGCGATGC TGATGTAGCT GCAGCGGCTT CACCACGCGA AGGACTTCCT TCTTTTCGGC

      9550       9560       9570       9580       9590       9600
CACATGACGC ATGTGGTGCT CACCGGCCGC AACGCGAAAG AAGACCTGAT CGAAGTCGCC
GTGTACTGCG TACACCACGA GTGGCCGGCG TTGCGCTTTC TTCTGGACTA GCTTCAGCGG
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FIG. 43P

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      9610       9620       9630       9640       9650       9660
GATCTCGTCA CTGAGATGGA GCTGATCAAG CATCCGTTCC GTTCCGGCAT CAAGGCGCAG
CTAGAGCAGT GACTCTACCT CGACTAGTTC GTAGGCAAGG CAAGGCCGTA GTTCCGCGTC

      9670       9680       9690       9700       9710       9720
CAGGGCGTGG AGTTCTGATG AGCCAGAGCT GGCAGTTCTG GGCGCTGCTT TCGGCCGCCT
GTCCCGCACC TCAAGACTAC TCGGTCTCGA CCGTCAAGAC CCGCGACGAA AGCCGGCGGA

      9730       9740       9750       9760       9770       9780
TCGCTGCGCT CACGGCGGTG TTTGCCAAGG TCGGGGTTGC GCAGATCAAC TCCGACTTCG
AGCGACGCGA GTGCCGCCAC AAACGGTTCC AGCCCCAACG CGTCTAGTTG AGGCTGAAGC

      9790       9800       9810       9820       9830       9840
CAACGCTGAT CCGCACCGTC GTCATCCTCT GCGTGATCGC CGCCATCGTG GCGGCGACAG
GTTGCGACTA GGCGTGGCAG CAGTAGGAGA CGCACTAGCG GCGGTAGCAC CGCCGCTGTC

      9850       9860       9870       9880       9890       9900
GGCAGTGGCA GAAGCCATCG GAAATCCCGG GCCGCACCTG GCTGTTCCTG GCGCTGTCAG
CCGTCACCGT CTTCGGTAGC CTTTAGGGCC CGGCGTGGAC CGACAAGGAC CGCGACAGTC

      9910       9920       9930       9940       9950       9960
GGCTTGCGAC TGGCGCTTCC TGGCTTGCCT ATTTCCGCGC GCTGAAGCTC GGCGACGCCG
CCGAACGCTG ACCGCGAAGG ACCGAACGGA TAAAGGCGCG CGACTTCGAG CCGCTGCGGC

      9970       9980       9990      10000      10010      10020
CCCGCGTGGC GCCGCTCGAC AAGCTCTCGA TCGTCATGGT CGCGATCTTC GGCGTGCTCT
GGGCGCACCG CGGCGAGCTG TTCGAGAGCT AGCAGTACCA GCGCTAGAAG CCGCACGAGA

     10030      10040      10050      10060      10070      10080
TCCTCGGTGA AAAGCTCAAC CTGATGAACT GGCTCGGCGT CGCCTTCATT GCCGCCGGGG
AGGAGCCACT TTTCGAGTTG GACTACTTGA CCGAGCCGCA GCGGAAGTAA CGGCGGCCCC

     10090      10100      10110      10120      10130      10140
CGCTGTTGCT GGCGGTGTTT TGAGCGCGCC TGCTCTGGTG CCTGTTCACT GAATGCTCGC
GCGACAACGA CCGCCACAAA ACTCGCGCGG ACGAGACCAC GGACAAGTGA CTTACGAGCG

     10150      10160      10170      10180      10190      10200
CTCAATCAAT CCGTAATCCC GACACATGCA GTGGTTGTGA CGAGCGGGAG GACGGCATGC
GAGTTAGTTA GGCATTAGGG CTGTGTACGT CACCAACACT GCTCGCCCTC CTGCCGTACG
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FIG. 43Q

10210	10220	10230	10240	10250	10260
AGATTGAAGG	CAATTGGAGC	GAGCGCCTTC	CTGATCCGTC	GGGCCACGTC	GCGCAGTTCG
TCTAACTTCC	GTTAACCTCG	CTCGCGGAAG	GACTAGGCAG	CCCGGTGCAG	CGCGTCAAGC
10270	10280	10290	10300	10310	10320
GCAGACGCTG	GAAGCGTCGC	AGCCTGAGGG	TGAGCCCTGC	TTCAGACCCA	CCGGCGGACA
CGTCTGCGAC	CTTCGCAGCG	TCGGACTCCC	ACTCGGGACG	AAGTCTGGGT	GGCCGCCTGT
10330	10340	10350	10360	10370	10380
CGCCTGCAAT	AGGCACCGTA	GGCGTCGCCG	AAGACCTTGG	CGAGGTGGGT	TTCCTCCATG
GCGGACGTTA	TCCGTGGCAT	CCGCAGCGGC	TTCTGGAACC	GCTCCACCCA	AAGGAGGTAC
10390	10400	10410	10420	10430	10440
CGGATCTGGT	AGGAAATCGA	GATCCAGGCG	GAGAGCGCCA	GCGCCACCGA	GATGACGTTG
GCCTAGACCA	TCCTTTAGCT	CTAGGTCCGC	CTCTCGCGGT	CGCGGTGGCT	CTACTGCAAC
10450	10460	10470	10480	10490	10500
GGCACCGCCA	TCACCGTGCC	GATCAGCGCG	GTCACCATGC	CGACATAGAT	CGGGTTGCGC
CCGTGGCGGT	AGTGGCACGG	CTAGTCGCGC	CAGTGGTACG	GCTGTATCTA	GCCCAACGCG
10510	10520	10530	10540	10550	10560
GAGAAGGCAT	AGAGGCCTGA	GGTCACAAGC	GGCGCGTCCT	GCTTTTCAGG	GATGCCGATC
CTCTTCCGTA	TCTCCGGACT	CCAGTGTTCG	CCGCGCAGGA	CGAAAAGTCC	CTACGGCTAG
10570	10580	10590	10600	10610	10620
TTCCAGGAAT	GACGCATCGC	CCATTGCGAC	AGCATCGTCA	GCCCGCCGCC	GAGCGTCATC
AAGGTCCTTA	CTGCGTAGCG	GGTAACGCTG	TCGTAGCAGT	CGGGCGGCGG	CTCGCAGTAG
10630	10640	10650	10660	10670	10680
AGCGCCAGGC	CGACGGCGTG	AAGGATGGGC	GTGTCGAGCG	CCGGGATCCG	GCCGAGGGCA
TCGCGGTCCG	GCTGCCGCAC	TTCCTACCCG	CACAGCTCGC	GGCCCTAGGC	CGGCTCCCGT
10690	10700	10710	10720	10730	10740
GCATCGACGG	AGGCCGGGAG	CATGGCGACC	GCCAGCAGGT	GGATCACCAG	CGCTGCGACG
CGTAGCTGCC	TCCGGCCCTC	GTACCGCTGG	CGGTCGTCCA	CCTAGTGGTC	GCGACGCTGC
10750	10760	10770	10780	10790	10800
ATCAGGCGGA	AAAGCCTGCC	CGCAAACCCT	TCCGCATCGT	CGCCATAGGT	TAGCACGACC
TAGTCCGCCT	TTTCGGACGG	GCGTTTGGGA	AGGCGTAGCA	GCGGTATCCA	ATCGTGCTGG

FIG. 43R

10810	10820	10830	10840	10850	10860
GGCGAGCGGC	CGGATTGCAC	GCGGCGGAGG	ATCGCCAGCG	CGAGCGTGGA	CAATCCCACG
CCGCTCGCCG	GCCTAACGTG	CGCCGCCTCC	TAGCGGTCGC	GCTCGCACCT	GTTAGGGTGC
10870	10880	10890	10900	10910	10920
ACGAGCATCA	GGATGGTGGG	AAGGGTGGTG	GACATGGAAA	CCTCTGGAGC	GAGCTGACAA
TGCTCGTAGT	CCTACCACCC	TTCCCACCAC	CTGTACCTTT	GGAGACCTCG	CTCGACTGTT
10930	10940	10950	10960	10970	10980
GACAGGAGCG	CACGACGGGT	AGGCGGCCCA	TATGAGCGTC	TACCCGGCGA	AGCATTCTGA
CTGTCCTCGC	GTGCTGCCCA	TCCGCCGGGT	ATACTCGCAG	ATGGGCCGCT	TCGTAAGACT
10990	11000	11010	11020	11030	11040
TCACCTTGCA	ATCTCTAGTA	ACTAGAGGTT	CAAGCGTCGG	ACCTGTCCGA	CTTTCGTCGT
AGTGGAACGT	TAGAGATCAT	TGATCTCCAA	GTTCGCAGCC	TGGACAGGCT	GAAAGCAGCA
11050	11060	11070	11080	11090	11100
GGTTACCGGA	TCTTATTGCC	AAGCGTTGGA	GGCTGTCATC	GTCGCCCCCG	CCGTGTCGGA
CCAATGGCCT	AGAATAACGG	TTCGCAACCT	CCGACAGTAG	CAGCGGGGGC	GGCACAGCCT
11110	11120	11130	11140	11150	11160
AGGTCGGCAA	AATTCGTCTC	TTGACGGCTG	CTCCTTCCGT	CGAGCGATTG	CATAGGCAGG
TCCAGCCGTT	TTAAGCAGAG	AACTGCCGAC	GAGGAAGGCA	GCTCGCTAAC	GTATCCGTCC
11170	11180	11190	11200	11210	11220
AGGCCGCACC	CATGTTAGAC	CGTCGACAGG	CTAAATACGG	GTGAACCTTG	AAGAATACTC
TCCGGCGTGG	GTACAATCTG	GCAGCTGTCC	GATTTATGCC	CACTTGGAAC	TTCTTATGAG
11230	11240	11250	11260	11270	11280
TCAGAGCTGC	GGTTGGTGTC	GCATCGGTCT	TGCTGTTCTT	GTCATCAGGT	GTGGCGGGGC
AGTCTCGACG	CCAACCACAG	CGTAGCCAGA	ACGACAAGAA	CAGTAGTCCA	CACCGCCCCG
11290	11300	11310	11320	11330	11340
AGGCGCAAAC	CGTGAAGAGC	GGGGCGTCAC	GAGCTCAAGA	AACGACGACC	ACCCAGAAGG
TCCGCGTTTG	GCACTTCTCG	CCCCGCAGTG	CTCGAGTTCT	TTGCTGCTGG	TGGGTCTTCC
11350	11360	11370	11380	11390	11400
CGAAACCGAA	AACTAAAACG	ACGCGCAAGC	AAAGGGCTGC	GGATGAAGCC	AAGGCCAAGG
GCTTTGGCTT	TTGATTTTGC	TGCGCGTTCG	TTTCCCGACG	CCTACTTCGG	TTCCGGTTCC

FIG. 43S

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     11410      11420      11430      11440      11450      11460
CGCTCGCCGA AGCGCGCCGT CCACGGATTT GCAAGACGCG GGAGAGCGAA TGCAGCTATG
GCGAGCGGCT TCGCGCGGCA GGTGCCTAAA CGTTCTGCGC CCTCTCGCTT ACGTCGATAC

     11470      11480      11490      11500      11510      11520
GCGCAGGTCC GGTCGGAGAG CAGTGCTCGT GCTGGTCGAA ATCCGGTGCG CCTGATCTTG
CGCGTCCAGG CCAGCCTCTC GTCACGAGCA CGACCAGCTT TAGGCCACGC GGACTAGAAC

     11530      11540      11550      11560      11570      11580
GCATAACTGT CAGGCGTTGA CCGCCCGCGA CCTTCGCGCG GGCAGGCAAG CGTGCGTCGC
CGTATTGACA GTCCGCAACT GGCGGGCGCT GGAAGCGCGC CCGTCCGTTC GCACGCAGCG

     11590      11600      11610      11620      11630      11640
TCGAAGCGAC GCCTGACGCG ATAGAAATCA CGGGTCGCCT GGTTCGTTCT GAAAGCTTGG
AGCTTCGCTG CGGACTGCGC TATCTTTAGT GCCCAGCGGA CCAAGCAAGA CTTTCGAACC

     11650      11660      11670      11680      11690      11700
GATTGGGTTT AGGTGATGGA AGCCGGCGTT GAACGCAAAA TAATGATCGA TCTCGAGAAC
CTAACCCAAA TCCACTACCT TCGGCCGCAA CTTGCGTTTT ATTACTAGCT AGAGCTCTTG

     11710      11720      11730      11740      11750      11760
AGCGCGCTCC AGTTTGCAAC CCGAGCACAC GGCGAACAGA AGCGTAAGTA TGACGGTCGG
TCGCGCGAGG TCAAACGTTG GGCTCGTGTG CCGCTTGTCT TCGCATTCAT ACTGCCAGCC

     11770      11780      11790      11800      11810      11820
CCCTATATCG TTCATCCGAT TGCGGTGGCG GAGATTGTTC GAAGCGTGCC CCATACGCCC
GGGATATAGC AAGTAGGCTA ACGCCACCGC CTCTAACAAG CTTCGCACGG GGTATGCGGG

     11830      11840      11850      11860      11870      11880
GAAATGATCG CCGCAGCGCT GCTTCACGAT ACGGTCGAAG ATACCGACGC GACGCTGCTG
CTTTACTAGC GGCGTCGCGA CGAAGTGCTA TGCCAGCTTC TATGGCTGCG CTGCGACGAC

     11890      11900      11910      11920      11930      11940
GAGATCAAGG AAGCGTTCGG CCCCAAGGTC GCAACACTGG TTGCGTGGCT CACCGACATA
CTCTAGTTCC TTCGCAAGCC GGGGTTCCAG CGTTGTGACC AACGCACCGA GTGGCTGTAT

     11950      11960      11970      11980      11990      12000
TCCACTCCGT TCCACGGCAA CCGACAGGTG CGCAAGGAAC TGGATCGCCA GCACCTCGCA
AGGTGAGGCA AGGTGCCGTT GGCTGTCCAC GCGTTCCTTG ACCTAGCGGT CGTGGAGCGT
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FIG. 43T

12010	12020	12030	12040	12050	12060
TCGGCGCCCG	CCGCGGCGAA	AACCGTCAAG	CTCGCCGACC	TGATCGACAA	TGCGATAGCG
AGCCGCGGGC	GGCGCCGCTT	TTGGCAGTTC	GAGCGGCTGG	ACTAGCTGTT	ACGCTATCGC
12070	12080	12090	12100	12110	12120
ATCAAAGCCG	GCGATCCGAA	TTTCTGGAAA	GTGTTCGGCG	CCGAGATGAA	ACGCTTGCTG
TAGTTTCGGC	CGCTAGGCTT	AAAGACCTTT	CACAAGCCGC	GGCTCTACTT	TGCGAACGAC
12130	12140	12150	12160	12170	12180
GAGGTCTTGG	GCGACGGCGA	CGAGACCCTT	CTCGCAAAGG	CCCGTGCATT	AGCGCCGGAA
CTCCAGAACC	CGCTGCCGCT	GCTCTGGGAA	GAGCGTTTCC	GGGCACGTAA	TCGCGGCCTT
12190	12200	12210	12220	12230	12240
TGAGAGTGCC	GCCGTTTATC	GGCAAGCATG	TCTGTGCCAT	GTCGACCCGG	TCAACCGGTC
ACTCTCACGG	CGGCAAATAG	CCGTTCGTAC	AGACACGGTA	CAGCTGGGCC	AGTTGGCCAG
12250	12260	12270	12280	12290	12300
ATCCAAGATC	GCAGAACGGA	CATGCATTTG	CGGTTTTGCC	CGCCGGTGTG	GCCCAGCCAC
TAGGTTCTAG	CGTCTTGCCT	GTACGTAAAC	GCCAAAACGG	GCGGCCACAC	CGGGTCGGTG
12310	12320	12330	12340	12350	12360
GCCTCACAGG	CTGCGCGGTT	GCGGCCGTTA	GGACAGCGCA	GAATTTGCCG	ACCGCGCCGC
CGGAGTGTCC	GACGCGCCAA	CGCCGGCAAT	CCTGTCGCGT	CTTAAACGGC	TGGCGCGGCG
12370	12380	12390	12400	12410	12420
GCCTCAATGC	CCCAGCCAGA	TCCGCAAGGG	ATGCGTCGGA	TCTGCGAGCA	GCCGGATCGC
CGGAGTTACG	GGGTCGGTCT	AGGCGTTCCC	TACGCAGCCT	AGACGCTCGT	CGGCCTAGCG
12430	12440	12450	12460	12470	12480
GAGCGCGATC	GAGACGATGA	CGAGCAGCGG	CTTGATGATC	TTGGCGCCCT	TGGCCATGGC
CTCGCGCTAG	CTCTGCTACT	GCTCGTCGCC	GAACTACTAG	AACCGCGGGA	ACCGGTACCG
12490	12500	12510	12520	12530	12540
ATAGCGCGAG	CCGACCTGGG	CGCCGAGGAA	CTGGCCGAGG	CCCATCAACA	GGCCGACCTT
TATCGCGCTC	GGCTGGACCC	GCGGCTCCTT	GACCGGCTCC	GGGTAGTTGT	CCGGCTGGAA
12550	12560	12570	12580	12590	12600
CCAGAGAACG	GCGCCGAAGA	AGAGGAAGAC	GCCGAAGGCG	CCGACGTTGG	AGCCAAAGTT
GGTCTCTTGC	CGCGGCTTCT	TCTCCTTCTG	CGGCTTCCGC	GGCTGCAACC	TCGGTTTCAA

FIG. 43U

```
     12610      12620      12630      12640      12650      12660
GAGGAACTTC GTGTGCGCCG TCGCCTTCAA CACGCCGAAG CCGGCGAGGG TAACGAAGCC
CTCCTTGAAG CACACGCGGC AGCGGAAGTT GTGCGGCTTC GGCCGCTCCC ATTGCTTCGG

     12670      12680      12690      12700      12710      12720
GAGCATGAAG AACGAGCCGG TGCCGGGGCC GAAGACGCCG TCATAAAAGC CGATTAGCGG
CTCGTACTTC TTGCTCGGCC ACGGCCCCGG CTTCTGCGGC AGTATTTTCG GCTAATCGCC

     12730      12740      12750      12760      12770      12780
CACCAGTGTC AGCGTGAAGA CGAAGGGGGT GACGCGGCTG TGCTGGTCGA CGTCGCCCAT
GTGGTCACAG TCGCACTTCT GCTTCCCCCA CTGCGCCGAC ACGACCAGCT GCAGCGGGTA

     12790      12800      12810      12820      12830      12840
GTTCGGCTTC AGGCCGAAAT AAAGCGCAAT GGCGATCAGC AGAAAGGGCA GGATCGCCTT
CAAGCCGAAG TCCGGCTTTA TTTCGCGTTA CCGCTAGTCG TCTTTCCCGT CCTAGCGGAA

     12850      12860      12870      12880      12890      12900
CAGCACGTCG CCGGGAACGA TGGTTGCGAG CAGGGCGCCG AGCACGGCGC CGGCGGCCGA
GTCGTGCAGC GGCCCTTGCT ACCAACGCTC GTCCCGCGGC TCGTGCCGCG GCCGCCGGCT

     12910      12920      12930      12940      12950      12960
CATCAGCGCC ATCGGCAGCT GCTCTTTCAG GTTCACGTGG CCGCGCCGGG CATAGGACAG
GTAGTCGCGG TAGCCGTCGA CGAGAAAGTC CAAGTGCACC GGCGCGGCCC GTATCCTGTC

     12970      12980      12990      13000      13010      13020
CGTGGCCGAG CCGGAGCCGA ACAATCCCTG CAGCTTGTTG GTGCCGAGCG TCTGCAAGGG
GCACCGGCTC GGCCTCGGCT TGTTAGGGAC GTCGAACAAC CACGGCTCGC AGACGTTCCC

     13030      13040      13050      13060      13070      13080
CGGGATGCCC GCAATGAGCA TGGCCGGAAT GGTGATCATG CCACCGCCGC CGGCGATCGA
GCCCTACGGG CGTTACTCGT ACCGGCCTTA CCACTAGTAC GGTGGCGGCG GCCGCTAGCT

     13090      13100      13110      13120      13130      13140
ATCGATGAAG CCTGCGATGA AGGCGGCGAC GAACAGGAAG GCGAGCAGGT GGAAGGCGAG
TAGCTACTTC GGACGCTACT TCCGCCGCTG CTTGTCCTTC CGCTCGTCCA CCTTCCGCTC

ATCT
TAGA
```

FIG. 43V

RESTRICTION MAP OF THE 13144-BP SEQUENCE

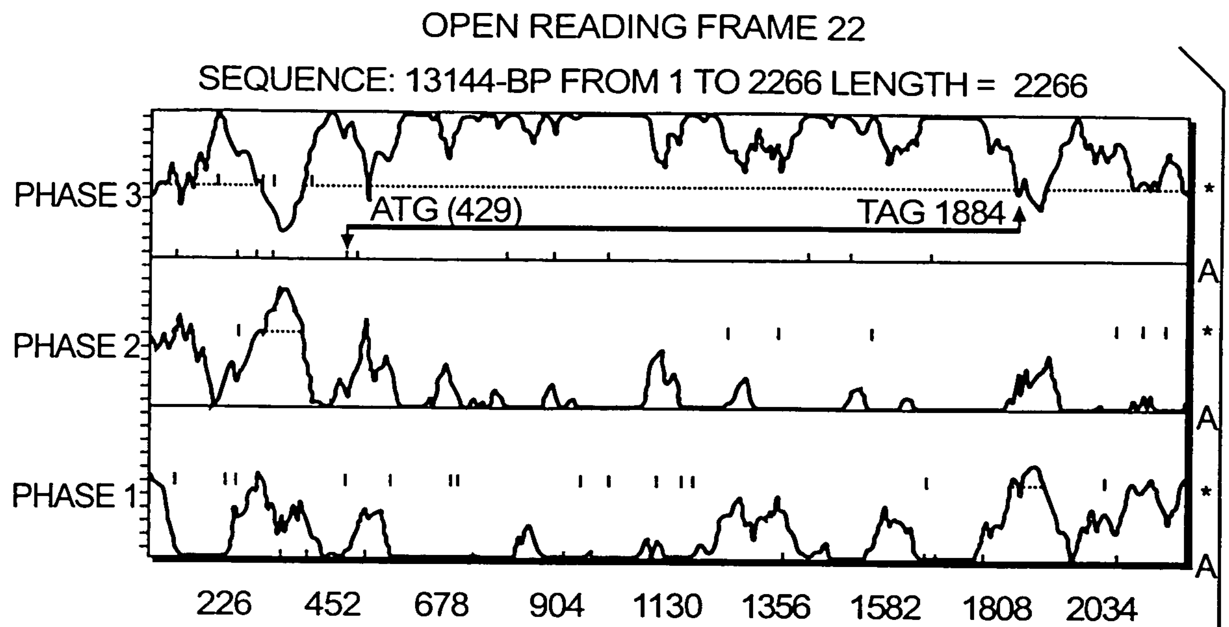
ApaLI	642,					
EcoRI	8818,					
HindIII	11633,					
MluI	7963,					
NdeI	10950,					
PvuII	12918,					
SfiI	3133,					
SplI	99,					
BglII	8248,	13139,				
KpnI	2315,	6300,				
NotI	5526,	7615,				
SmaI	1322,	9868,				
SspI	4843,	6968,				
XmnI	9313,	12091,				
AatII	1033,	9503,	12773,			
AflIII	550,	7963,	8634,			
BalI	2107,	6236,	12473,			
BamHI	2266,	5416,	10664,			
BspMII	5002,	8494,	8914,			
EcoRV	4263,	4605,	5137,			
NcoI	6318,	7786,	12474,			
NsiI	3467,	5064,	12266,			
PflMI	7870,	10718,	11065,			
XhoI	1512,	4171,	11692,			
ApaI	1928,	3138,	3386,	8551,		
AsuII	784,	5670,	8418,	11799,		
FspII	784,	5670,	8418,	11799,		
MaeI	1883,	2647,	10995,	11002,		
NruI	1827,	3794,	10002,	12419,		
SauI	852,	7001,	10284,	10517,		
BstEII	995,	3642,	8456,	10470,	11041,	
Eco47III	6954,	7209,	8434,	10731,	11837,	
SacI	5,	4109,	4694,	5169,	11315,	
StuI	204,	4081,	8261,	9406,	10515,	
BstXI	761,	2982,	3612,	6031,	6232,	9102,
SacII	932,	1025,	2096,	3537,	5184,	12014,
SphI	966,	2740,	5360,	8098,	9246,	10199,

FIG. 44A

RESTRICTION MAP OF THE 13144-BP SEQUENCE

BclI	2992,	4016,	9029,	9164,	9623,	10978,	13053,	
RsaI	101,	1201,	1918,	2313,	4881,	6298,	6856,	
Tth111I	1821,	2424,	4351,	7361,	7904,	12227,	12697,	
PstI	613,	3989,	5832,	5952,	7260,	7782,	8211,	12992,
ClaI	1351,	3596,	4469,	4724,	5748,	6618,	8574,	11687,
	13082,							
FspI	1363,	1551,	1653,	5219,	7841,	7982,	8342,	9760,
	11971,							
HinfI	1137,	2564,	2592,	3025,	5667,	5927,	6467,	6923,
	13079,							
StyI	2488,	3396,	5116,	6105,	6318,	7786,	9745,	10355,
	11389,	11395,	11903,	12468,	12474,			
DdeI	852,	1875,	3373,	3586,	6311,	7001,	7010,	7610,
	8956,	9020,	9611,	10284,	10517,	11220,		
Nsp7524I	554,	966,	2394,	2740,	5360,	7840,	8098,	8638,
	9246,	9553,	10168,	10199,	12210,	12264,		
PvuI	26,	1853,	2453,	4403,	4703,	4728,	5091,	5112,
	5178,	6717,	7269,	9991,	12429,	13077,		
AvaI	975,	1320,	1503,	1512,	3131,	3231,	3709,	3766,
	4171,	4212,	7224,	7573,	9866,	11692,	11720,	
BanII	5,	496,	1723,	1928,	2254,	3138,	3386,	4109,
	4694,	5196,	6207,	6282,	8551,	10296,	11315,	
SalI	83,	1296,	2418,	4045,	4303,	5258,	6959,	7700,
	7967,	8627,	8708,	9198,	11182,	12221,	12766,	
XhoII	2266,	3920,	5416,	5688,	6943,	7020,	7140,	8248,
	10382,	10400,	10664,	11048,	12378,	12398,	13139,	

FIG. 44B


OPEN READING FRAME 22
SEQUENCE: 13144-BP FROM 1 TO 2266 LENGTH = 2266
PHASE 3
PHASE 2
PHASE 1
ATG (429)
TAG 1884
226
452
678
904
1130
1356
1582
1808
2034

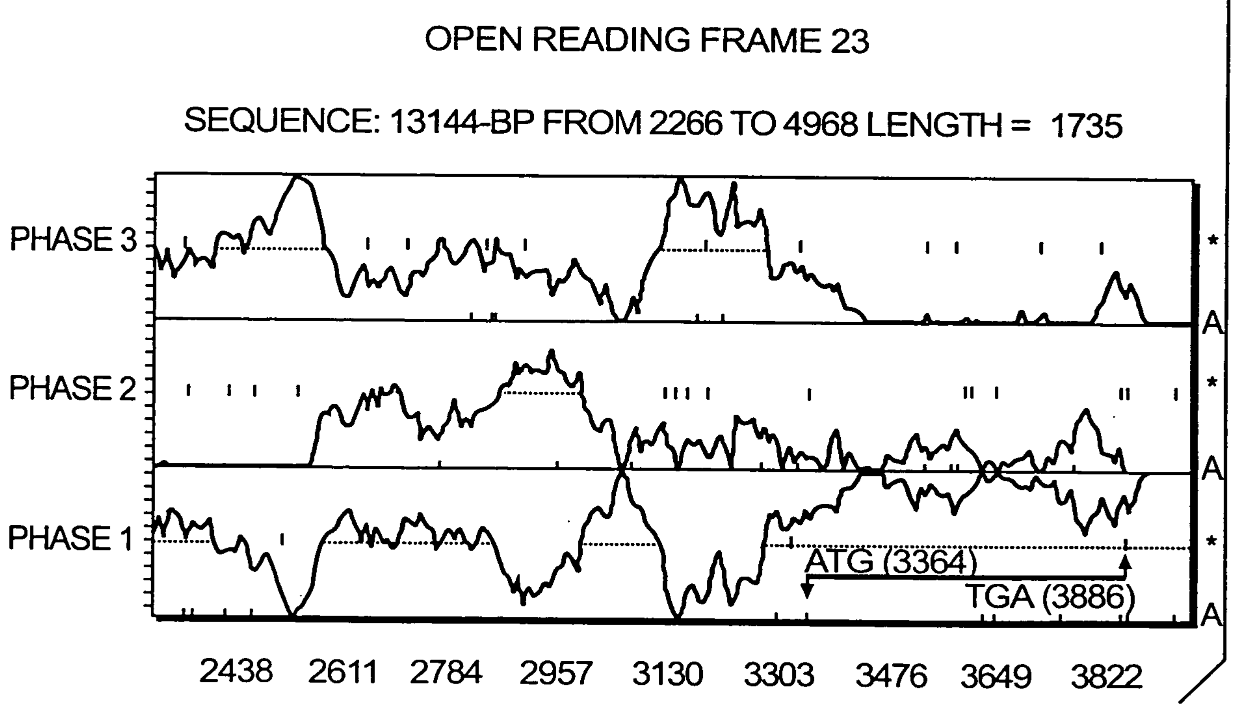
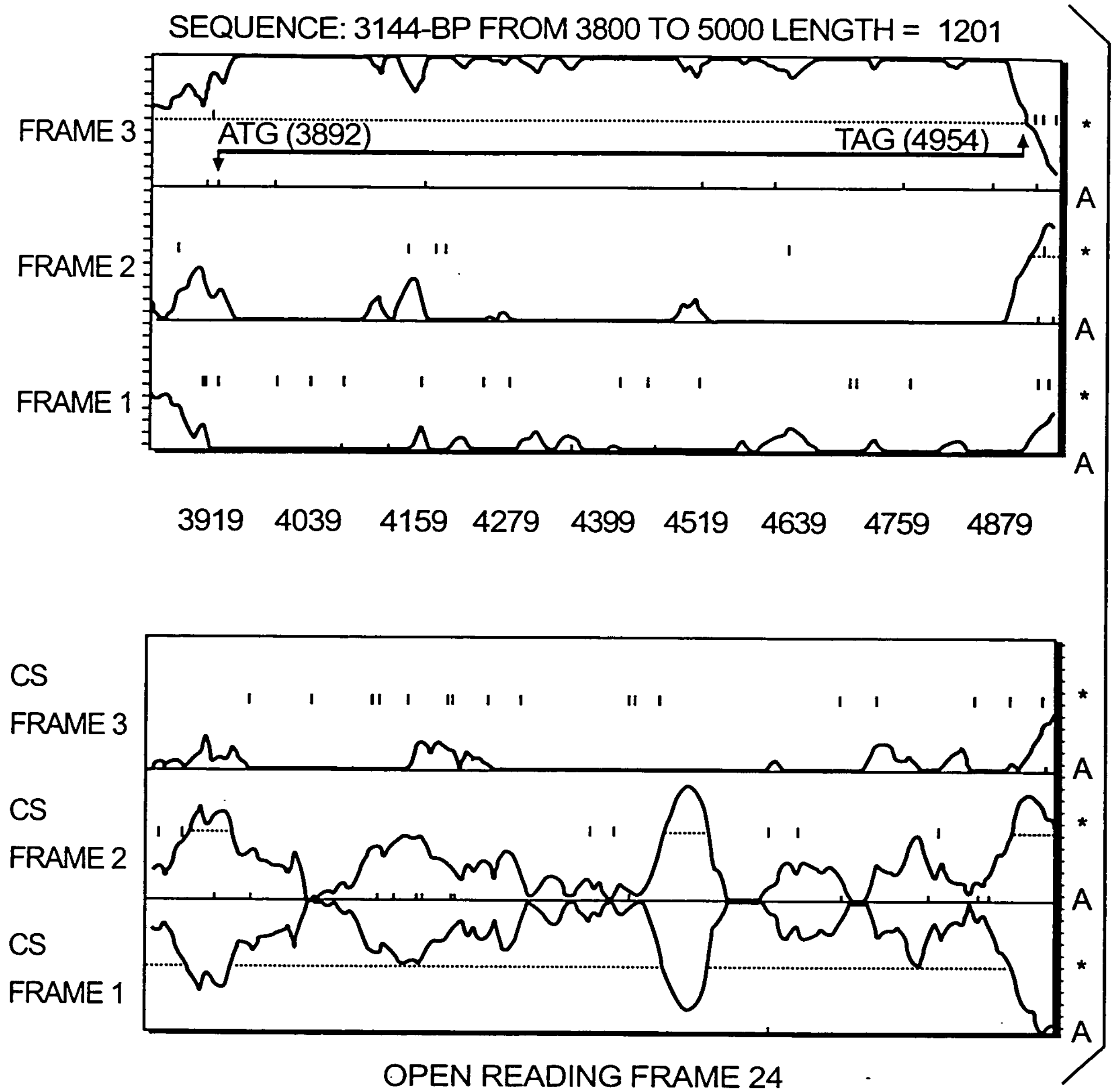

OPEN READING FRAME 23
SEQUENCE: 13144-BP FROM 2266 TO 4968 LENGTH = 1735
PHASE 3
PHASE 2
PHASE 1
ATG (3364)
TGA (3886)
2438
2611
2784
2957
3130
3303
3476
3649
3822

FIG. 45A



OPEN READING FRAME 24

FIG. 45B

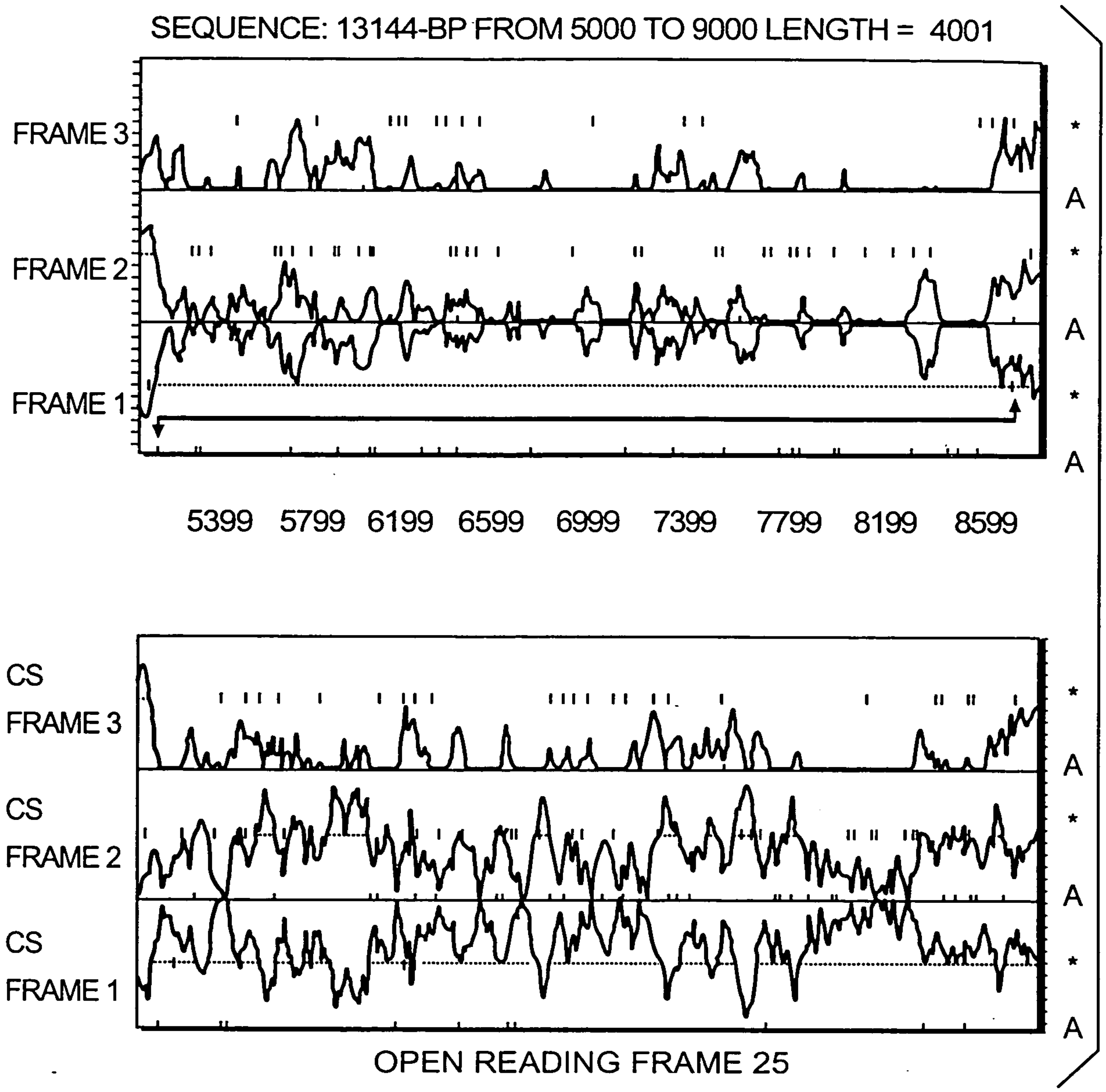

SEQUENCE: 13144-BP FROM 5000 TO 9000 LENGTH = 4001
FRAME 3
FRAME 2
FRAME 1
5399
5799
6199
6599
6999
7399
7799
8199
8599
CS
FRAME 3
CS
FRAME 2
CS
FRAME 1
OPEN READING FRAME 25

FIG. 45C

SEQUENCE: 1344-BP FROM 9000 TO 9700 LENGTH = 701

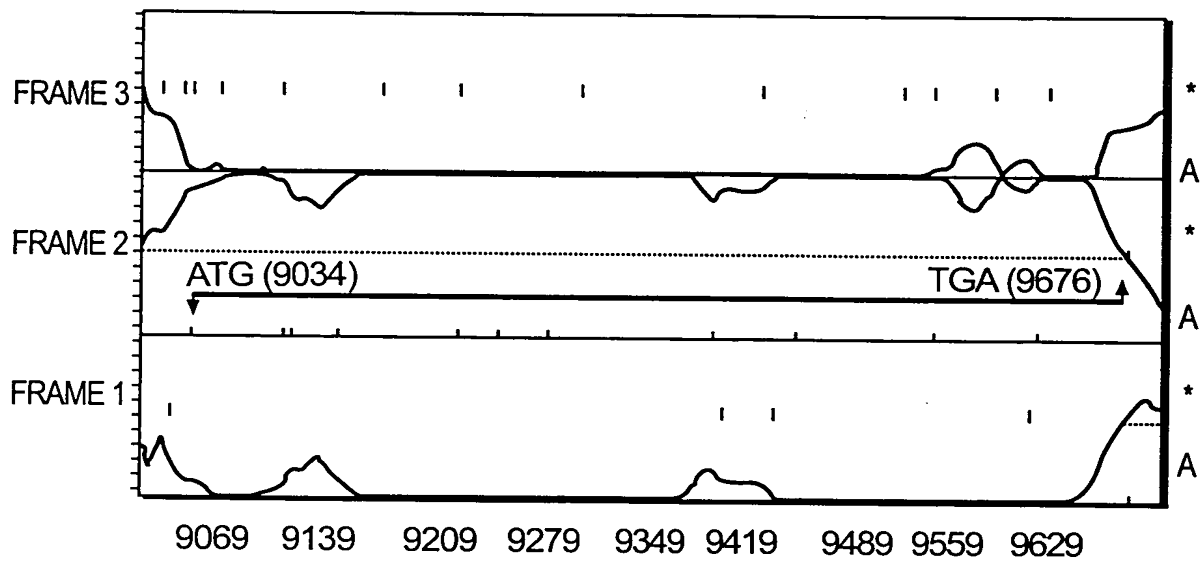
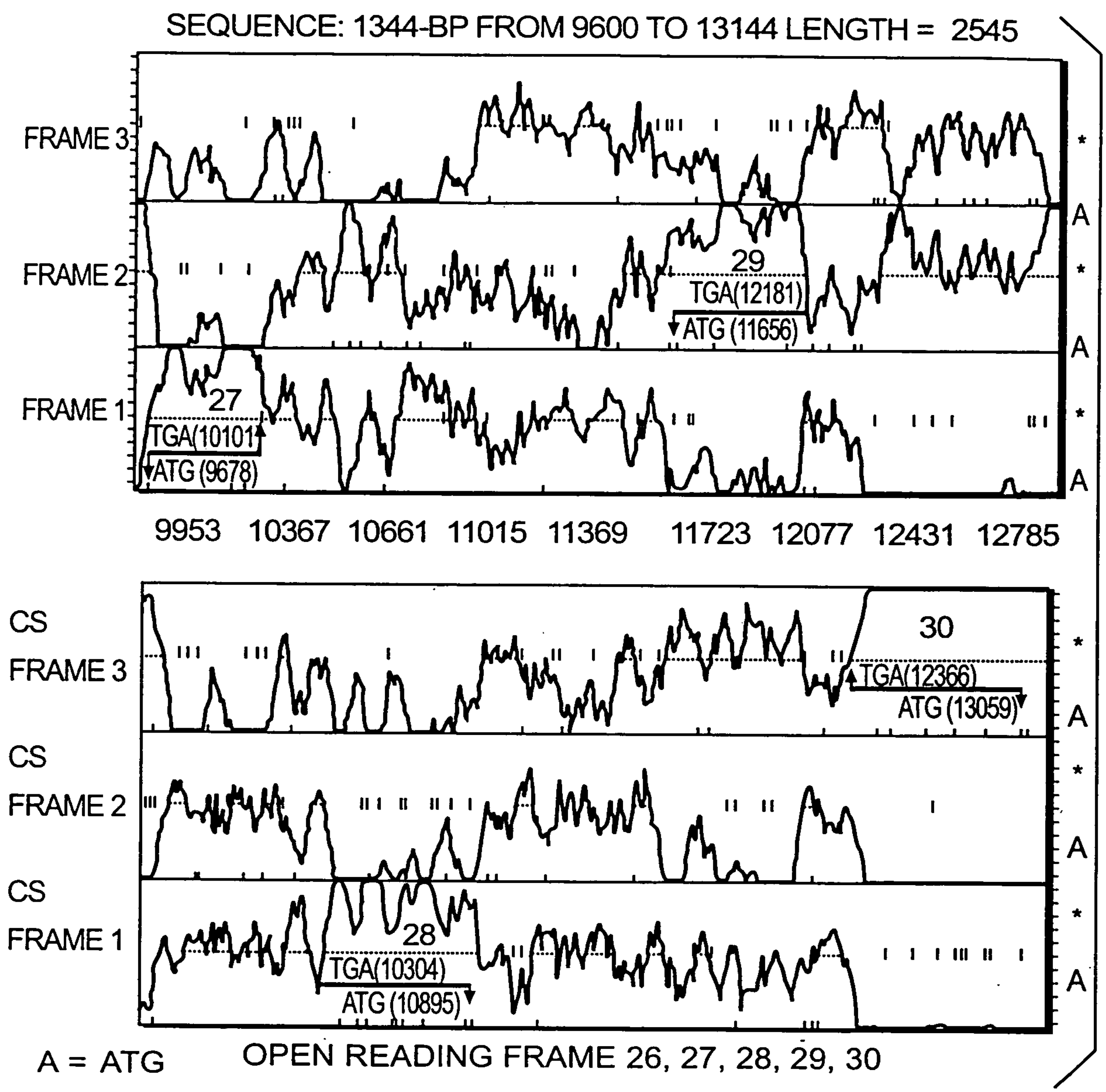


FIG. 45D



A = ATG OPEN READING FRAME 26, 27, 28, 29, 30

*: STOP CODON

CS: COMPLEMENTARY STRAND

FIG. 45E

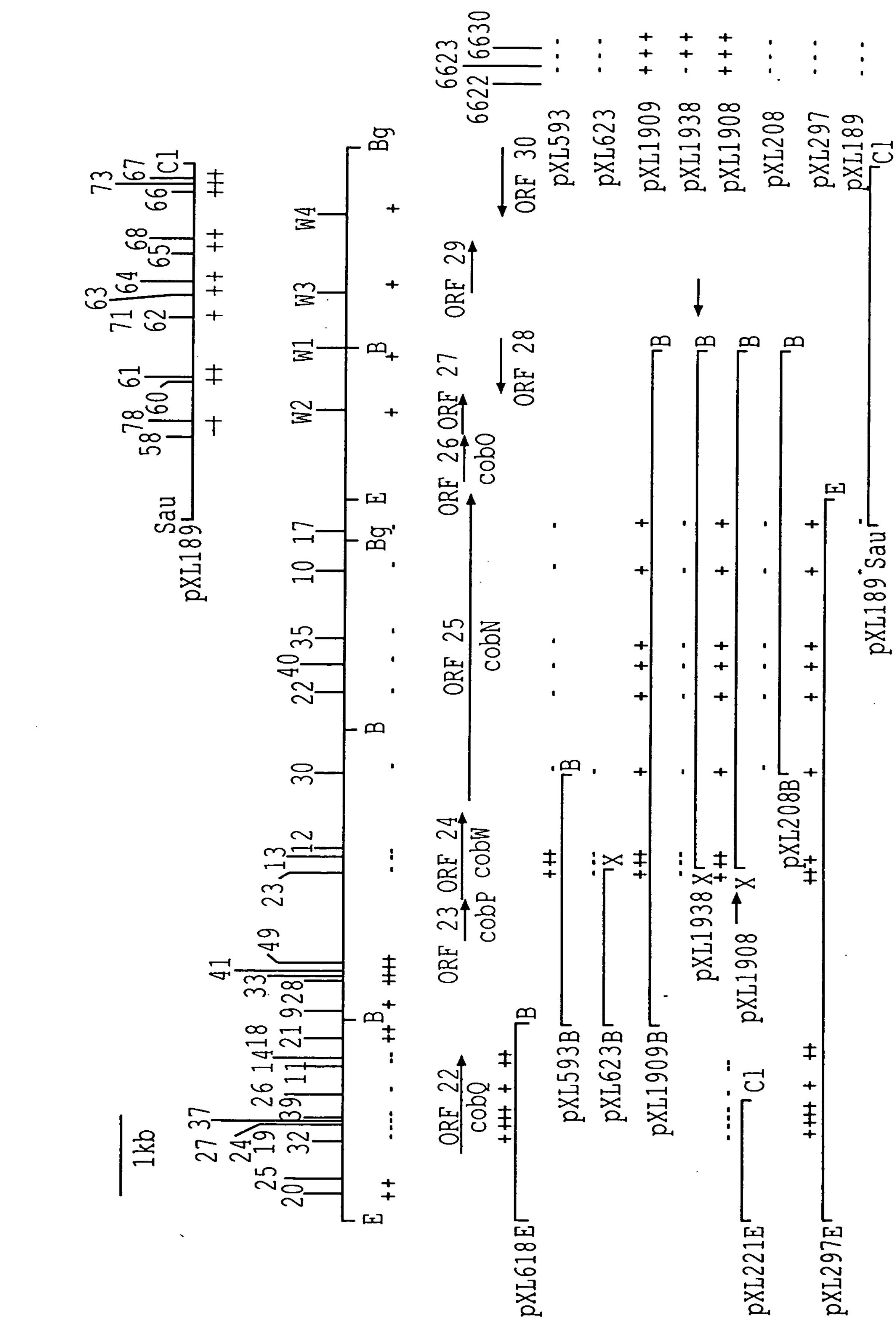

1kb
pXL189
Sau
ORF 22
cobQ
ORF 23
cobP
ORF 24
cobW
ORF 25
cobN
ORF 26
cobO
ORF 27
ORF 28
ORF 29
ORF 30
pXL618
pXL593
pXL623
pXL1909
pXL221
pXL1938
pXL1908
pXL208
pXL297
6622
6623
6630

FIG. 46

13144-BP SEQUENCE FROM 429 TO 1328 <u>cobQ</u> GENE

```
 M  T  R  R  I  M  L  Q  G  T  G  S  D  V  G  K  S  V  L  V  A  G  L  C  R
 ATGACACGCAGGATCATGTTGCAGGGAACCGGCTCGGATGTCGGAAAATCGGTATTGGTGGCGGGGCTCTGCCGG
429       439       449       459       469       479       489       499
 L  A  A  N  Q  G  L  K  V  R  P  F  K  P  Q  N  M  S  N  N  A  A  V  S  D
 CTTGCCGCCAATCAGGGCCTGAAGGTCCGGCCGTTCAAGCCGCAGAACATGTCGAACAACGCCGCCGTTTCCGAC
504       514       524       534       544       554       564       574
 D  G  G  E  I  G  R  A  Q  W  L  Q  A  L  A  A  R  V  P  S  S  V  H  M  N
 GACGGCGGCGAGATCGGCCGCGCGCAATGGCTGCAGGCGCTGGCCGCGCGCGTGCCGTCGTCGGTGCACATGAAC
579       589       599       609       619       629       639       649
 P  V  L  L  K  P  Q  S  D  V  G  S  Q  I  V  V  Q  G  K  V  A  G  Q  A  R
 CCGGTGCTCCTGAAGCCGCAGTCGGACGTGGGCAGCCAGATCGTCGTTCAGGGCAAGGTCGCCGGGCAGGCCAGG
654       664       674       684       694       704       714       724
 G  R  E  Y  Q  A  L  K  P  K  L  L  G  A  V  M  E  S  F  E  Q  I  S  A  G
 GGGCGGGAATATCAGGCGCTCAAGCCCAAGCTGCTGGGCGCCGTCATGGAGAGTTTCGAACAAATATCGGCCGGT
729       739       749       759       769       779       789       799
 A  D  L  V  V  V  E  G  A  G  S  P  A  E  I  N  L  R  P  G  D  I  A  N  M
 GCCGATCTCGTGGTGGTCGAAGGCGCCGGCTCGCCGGCCGAAATCAACCTCAGGCCCGGCGACATCGCCAATATG
804       814       824       834       844       854       864       874
 G  F  A  T  R  A  N  V  P  V  V  L  V  G  D  I  D  R  G  G  V  I  R  S  L
 GGCTTTGCGACACGGGCCAATGTGCCGGTCGTGCTGGTCGGCGACATCGACCGCGGGGGGGTGATCGCCTCGCTG
879       889       899       909       919       929       939       949
 V  G  T  H  A  I  L  P  E  E  D  R  R  M  V  T  G  Y  L  I  N  K  F  R  G
 GTCGGCACGCATGCGATCCTGCCCGAGGAAGACCGGCGCATGGTGACCGGCTATCTCATCAACAAGTTCCGCGGC
954       964       974       984       994      1004      1014      1024
 D  V  T  L  F  D  D  G  I  A  A  V  N  R  Y  T  G  W  P  C  F  G  V  V  P
 GACGTCACGCTGTTCGACGACGGCATTGCTGCCGTCAACCGCTACACCGGCTGGCCCTGCTTCGGCGTCGTGCCG
1029      1039      1049      1059      1069      1079      1089      1099
 W  L  K  A  A  A  R  L  P  A  E  D  S  V  V  L  E  K  L  T  R  G  E  G  R
 TGGCTGAAGGCGGCGGCACGCCTGCCGGCGGAAGATTCCGTCGTGCTGGAGAAGCTGACGCGCGGCGAGGGGCGG
1104      1114      1124      1134      1144      1154      1164      1174
 A  L  K  V  A  V  P  V  L  S  R  I  A  N  F  D  D  L  D  P  L  A  A  E  P
 GCGCTGAAGGTTGCCGTCCCGGTACTGTCGCGCATCGCCAATTTCGACGACCTCGATCCGCTCGCCGCCGAACCG
1179      1189      1199      1209      1219      1229      1239      1249
 E  I  D  L  V  F  V  R  P  G  S  P  I  P  V  D  A  G  L  V  V  I  P  G  S
 GAGATTGATCTCGTCTTCGTGCGGCCTGGCAGTCCCATTCCGGTCGACGCTGGCCTCGTCGTCATTCCCGGGTCG
1254      1264      1274      1284      1294      1304      1314      1324
```

FIG. 47A

13144-BP SEQUENCE FROM 1329 TO 1886 <u>cobQ</u> GENE

```
 K  S  T  I  G  D  L  I  D  F  R  A  Q  G  W  D  R  D  L  E  R  H  V  R  R
  AAATCGACCATCGGCGACCTCATCGATTTCCGTGCGCAAGGGTGGGACCGTGACCTCGAACGTCATGTGCGCCGG
1329      1339      1349      1359      1369      1379      1389      1399
 G  G  R  V  I  G  I  C  G  G  Y  Q  M  L  G  R  R  V  T  D  P  L  G  I  E
  GGCGGCCGGGTCATCGGCATCTGCGGCGGCTACCAGATGCTCGGCCGGCGCGTCACCGATCCGCTCGGCATCGAG
1404      1414      1424      1434      1444      1454      1464      1474
 G  G  E  R  A  V  E  G  L  G  L  L  E  V  E  T  E  M  A  P  E  K  T  V  R
  GGCGGCGAACGTGCGGTCGAGGGCCTCGGGCTGCTCGAGGTCGAGACCGAGATGGCGCCGGAAAAGACGGTGCGC
1479      1489      1499      1509      1519      1529      1539      1549
 N  S  R  A  W  S  L  E  H  D  V  V  L  E  G  Y  E  I  H  L  G  K  T  Q  G
  AACAGCCGCGCCTGGTCGCTGGAGCATGATGTGGTGCTCGAAGGCTACGAAATCCATCTTGGCAAGACGCAAGGT
1554      1564      1574      1584      1594      1604      1614      1624
 A  D  C  G  R  P  S  V  R  I  D  N  R  A  D  G  A  L  S  A  D  G  R  V  M
  GCGGACTGTGGCCGGCCGTCGGTGCGCATCGACAATCGCGCCGACGGCGCCCTTTCGGCCGATGGCCGCGTGATG
1629      1639      1649      1659      1669      1679      1689      1699
 G  T  Y  L  H  G  L  F  T  S  D  A  Y  R  G  A  L  L  K  S  F  G  I  E  G
  GGCACCTACCTGCATGGGCTCTTCACCAGCGACGCCTATCGCGGCGCGCTGCTCAAGAGTTTCGGCATCGAAGGC
1704      1714      1724      1734      1744      1754      1764      1774
 G  A  N  N  Y  R  Q  S  V  D  A  A  L  D  D  V  A  N  E  L  E  A  V  L  D
  GGCGCCAACAACTACCGCCAATCGGTCGATGCGGCGCTCGACGATGTCGCGAACGAACTGGAGGCTGTGCTCGAT
1779      1789      1799      1809      1819      1829      1839      1849
 R  R  W  L  D  E  L  L  R  H  *  (SEQ ID NO:43)
 CGTCGCTGGCTGGACGAGTTGCTCAGGCACTAG (SEQ ID NO:42)
1854      1864      1874      1884
```

FIG. 47B

COBQ PROTEIN

FIRST RESIDUE = 1
LAST RESIDUE = 485

			NUMBER	NO.%	WEIGHT	WEIGHT %
1	PHE	F	11	2.27	1617.75	3.11
2	LEU	L	50	10.31	5654.20	10.88
3	ILE	I	23	4.74	2600.93	5.01
4	MET	M	10	2.06	1310.41	2.52
5	VAL	V	50	10.31	4953.42	9.53
6	SER	S	24	4.95	2088.77	4.02
7	PRO	P	23	4.74	2232.21	4.30
8	THR	T	15	3.09	1515.72	2.92
9	ALA	A	49	10.10	3480.82	6.70
10	TYR	Y	8	1.65	1304.51	2.51
11	*	*	0	0.00	0.00	0.00
12	HIS	H	7	1.44	959.41	1.85
13	GLN	Q	15	3.09	1920.88	3.70
14	ASN	N	16	3.30	1824.69	3.51
15	LYS	K	15	3.09	1921.42	3.70
16	ASP	D	34	7.01	3910.92	7.53
17	GLU	E	28	5.77	3613.19	6.96
18	CYS	C	4	0.82	412.04	0.79
19	TRP	W	6	1.24	1116.48	2.15
20	ARG	R	40	8.25	6244.04	12.02
21	GLY	G	57	11.75	3250.22	6.26
22	-	-	0	0.00	0.00	0.00

RESIDUES = 485
MOLECULAR WEIGHT (MONOISOTOPIC) = 51950.1016
MOLECULAR WEIGHT (AVERAGE) = 51982.3711
INDEX OF POLARITY (%) = 40.00
ISOELECTRIC POINT = 6.16
OD 260 (1mg/ml) = 0.558 OD 280 (1mg/ml) = 0.825

COBQ FROM 1 TO 485

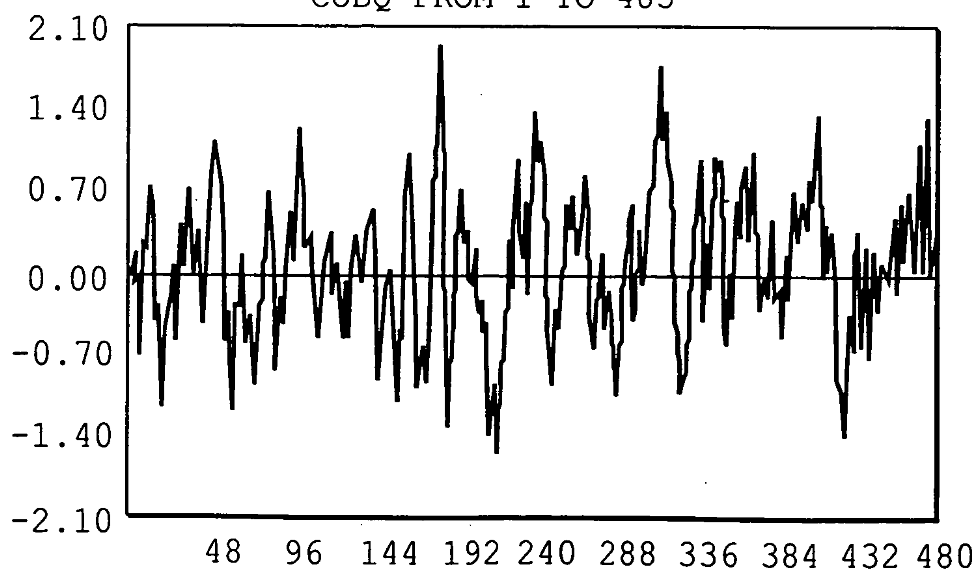


FIG. 47C

13144-BP SEQUENCE FROM 3364 TO 3888 cobP GENE

```
   M  S  S  L  S  A  G  P  V  L  V  L  G  G  A  R  S  G  K  S  S  F  S  E  R
    ATGAGCAGTCTCAGCGCCGGGCCCGTGCTGGTCCTTGGCGGCGCCCGTTCCGGCAAGTCCAGCTTTTCCGAGAGG
3364      3374      3384      3394      3404      3414      3424      3434
   L  V  E  A  S  G  F  T  M  H  Y  V  A  T  G  R  A  W  D  D  E  M  R  E  R
    CTCGTCGAAGCGTCCGGCTTCACCATGCATTATGTCGCCACGGGCCGCGCCTGGGACGACGAAATGCGCGAGCGC
3439      3449      3459      3469      3479      3489      3499      3509
   I  D  H  H  R  T  R  R  G  E  G  W  T  T  H  E  E  P  L  D  L  V  G  I  L
    ATCGACCATCACCGGACGCGCCGCGGCGAGGGCTGGACGACGCATGAGGAGCCGCTCGATCTCGTCGGCATCCTC
3514      3524      3534      3544      3554      3564      3574      3584
   R  R  I  D  D  P  S  H  V  V  L  I  D  C  L  T  L  W  V  T  N  L  M  L  E
    AGACGCATCGATGATCCCAGCCATGTGGTCCTGATCGACTGCCTGACGCTATGGGTCACCAATCTCATGCTGGAA
3589      3599      3609      3619      3629      3639      3649      3659
   E  R  D  M  T  A  E  F  A  A  L  V  A  Y  L  P  E  A  R  A  R  L  V  F  V
    GAGCGCGACATGACGGCGGAGTTCGCCGCCCTTGTTGCGTATCTGCCCGAGGCGCGGGCGCGCCTCGTCTTTGTT
3664      3674      3684      3694      3704      3714      3724      3734
   S  N  E  V  G  L  G  I  V  P  E  N  R  M  A  R  E  F  R  D  H  A  G  R  L
    TCCAATGAGGTCGGCCTCGGCATCGTGCCCGAGAACCGCATGGCCCGCGAGTTTCGCGACCATGCCGGCCGGCTT
3739      3749      3759      3769      3779      3789      3799      3809
   H  Q  I  V  A  E  K  S  A  E  V  Y  F  V  R  A  G  L  P  L  K  M  K  G  *
    CACCAGATCGTTGCGGAGAAATCCGCTGAAGTTTACTTTGTCGCGGCCGGTTTGCCGCTGAAAATGAAGGGTTGA
3814      3824      3834      3844      3854      3864      3874      3884
(SEQ ID NO: 45)
(SEQ ID NO: 44)
```

FIG. 47D

COBP PROTEIN FIRST RESIDUE = 1
LAST RESIDUE = 174

			NUMBER	NO.%	WEIGHT	WEIGHT %
1	PHE	F	6	3.45	882.41	4.54
2	LEU	L	19	10.92	2148.60	11.06
3	ILE	I	6	3.45	678.50	3.49
4	MET	M	7	4.02	917.28	4.72
5	VAL	V	16	9.20	1585.09	8.16
6	SER	S	11	6.32	957.35	4.93
7	PRO	P	6	3.45	582.32	3.00
8	THR	T	8	4.60	808.38	4.16
9	ALA	A	17	9.77	1207.63	6.22
10	TYR	Y	3	1.72	489.19	2.52
11	*	*	0	0.00	0.00	0.00
12	HIS	H	7	4.02	959.41	4.94
13	GLN	Q	1	0.57	128.06	0.66
14	ASN	N	3	1.72	342.13	1.76
15	LYS	K	4	2.30	512.38	2.64
16	ASP	D	9	5.17	1035.24	5.33
17	GLU	E	16	9.20	2064.68	10.63
18	CYS	C	1	0.57	103.01	0.53
19	TRP	W	3	1.72	558.24	2.87
20	ARG	R	17	9.77	2653.72	13.66
21	GLY	G	14	8.05	798.30	4.11
22	-	-	0	0.00	0.00	0.00

RESIDUES = 174
MOLECULAR WEIGHT (MONOISOTOPIC) = 19429.9473
MOLECULAR WEIGHT (AVERAGE) = 19442.2637
INDEX OF POLARITY (%) = 43.68
ISOELECTRIC POINT = 6.71
OD 260 (1mg/ml) = 0.720 OD 280 (1mg/ml) = 1.042

COBP FROM 1 TO 174

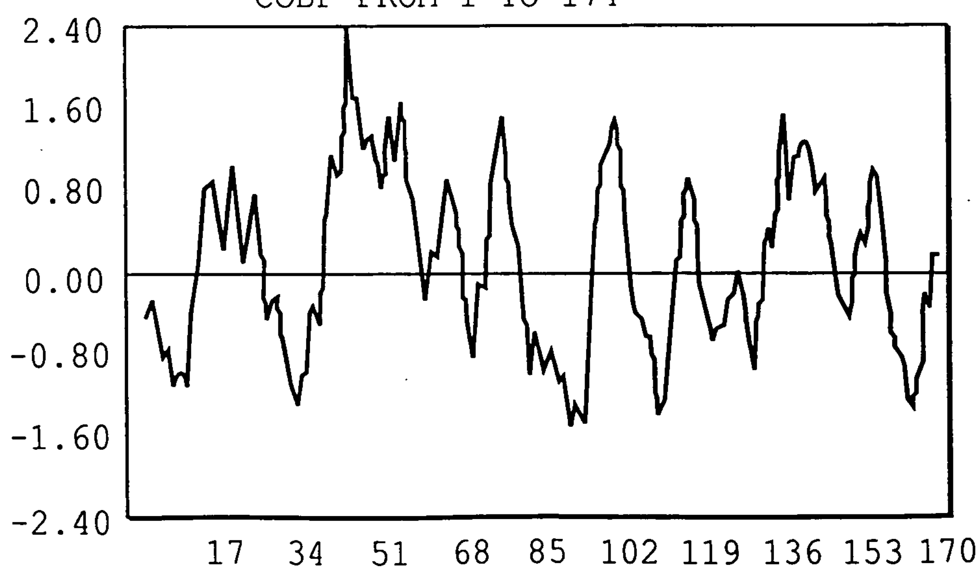


FIG. 47E

13144-BP SEQUENCE FROM 3892 TO 4956 cobW GENE

```
   M  T  T  A  R  A  N  Q  G  K  I  P  A  T  V  I  T  G  F  L  G  A  G  K  T
   ATGACCACTGCGAGAGCCAACCAGGGCAAGATCCCGGCGACCGTCATCACCGGCTTCCTCGGCGCCGGCAAGACG
3892      3902      3912      3922      3932      3942      3952      3962
   T  M  I  R  N  L  L  Q  N  A  D  G  K  R  I  G  L  I  I  N  E  F  G  D  L
   ACGATGATCCGCAACCTGCTGCAGAACGCCGACGGCAAGCGCATCGGCCTGATCATCAACGAGTTCGGCGATCTT
3967      3977      3987      3997      4007      4017      4027      4037
   G  V  D  G  D  V  L  K  G  C  G  A  E  A  C  T  E  D  D  I  I  E  L  T  N
   GGCGTCGACGGCGATGTCTTGAAGGGCTGCGGTGCCGAGGCCTGCACCGAGGACGACATCATCGAGCTCACCAAT
4042      4052      4062      4072      4082      4092      4102      4112
   G  C  I  C  C  T  V  A  D  D  F  I  P  T  M  T  K  L  L  E  R  E  N  R  P
   GGCTGCATCTGCTGCACCGTGGCTGACGATTTCATCCCGACCATGACGAAGCTGCTCGAGCGTGAAAACCGTCCT
4117      4127      4137      4147      4157      4167      4177      4187
   D  H  I  I  I  E  T  S  G  L  A  L  P  Q  P  L  I  A  A  F  N  W  P  D  I
   GACCACATCATCATCGAAACCTCGGGCCTTGCCCTGCCGCAGCCGCTGATCGCCGCTTTCAACTGGCCGGATATC
4192      4202      4212      4222      4232      4242      4252      4262
   R  S  E  V  T  V  D  G  V  V  T  V  V  D  S  A  A  V  A  A  G  R  F  A  D
   CGCAGCGAAGTGACCGTCGATGGCGTCGTCACCGTGGTCGACAGCGCCGCCGTTGCCGCTGGCCGCTTTGCCGAC
4267      4277      4287      4297      4307      4317      4327      4337
   D  H  D  K  V  D  A  L  R  V  E  D  D  N  L  D  H  E  S  P  I  E  E  L  F
   GACCACGACAAGGTCGATGCGCTGCGCGTCGAGGACGACAATCTCGATCACGAAAGCCCGATCGAGGAGCTGTTC
4342      4352      4362      4372      4382      4392      4402      4412
   E  D  Q  L  T  A  A  D  L  I  V  L  N  K  T  D  L  I  D  A  S  G  L  K  A
   GAGGATCAACTGACGGCTGCCGATCTCATCGTTCTCAACAAGACCGATCTGATCGATGCCTCCGGCCTCAAGGCC
4417      4427      4437      4447      4457      4467      4477      4487
   V  R  D  E  V  S  S  R  T  S  R  K  P  T  M  I  E  A  K  N  G  E  V  A  A
   GTGCGCGACGAGGTGTCTTCGCGCACCAGCCGCAAGCCCACGATGATCGAGGCGAAAAACGGCGAAGTCGCCGCT
4492      4502      4512      4522      4532      4542      4552      4562
   A  I  L  L  G  L  G  V  G  T  E  S  D  I  A  N  R  K  S  H  H  E  M  E  H
   GCCATCCTGCTTGGCCTCGGTGTCGGCACGGAAAGCGATATCGCCAACCGCAAGTCGCATCACGAGATGGAGCAC
4567      4577      4587      4597      4607      4617      4627      4637
   E  A  G  E  E  H  D  H  D  E  F  D  S  F  V  V  E  L  G  S  I  A  D  P  A
   GAGGCAGGTGAGGAGCACGATCACGACGAGTTCGACAGCTTCGTCGTCGAGCTCGGTTCGATCGCCGATCCGGCC
4642      4652      4662      4672      4682      4692      4702      4712
   A  F  I  D  R  L  K  G  V  I  A  E  H  D  V  L  R  L  K  G  F  A  D  V  P
   GCCTTCATCGATCGCCTGAAGGGCGTAATCGCGGAGCACGACGTTCTGCGCCTCAAGGGTTTTGCAGACGTGCCC
4717      4727      4737      4747      4757      4767      4777      4787
```

FIG. 47F

```
   G  K  P  M  R  L  L  I  Q  R  V  G  A  R  I  D  Q  Y  Y  D  R  A  W  G  A
    GGCAAGCCGATGCGCCTCCTGATCCAGGCGGTCGGCGCCCGCATCGACCAATATTACGACCGCGCCTGGGGCGCT
4792      4802      4812      4822      4832      4842      4852      4862
   G  E  K  R  G  T  R  L  V  V  I  G  L  H  D  M  D  E  A  A  V  R  A  A  I
    GGCGAAAAGCGCGGTACGCGCCTCGTCGTCATCGGCCTGCACGACATGGACGAGGCGGCGGTGCGCGCCGCGATC
4867      4877      4887      4897      4907      4917      4927      4937
   T  A  L  V  *    (SEQ. ID. NO: 47)
    ACCGCGCTCGTGTAG (SEQ. ID. NO: 46)
4942      4952
```

FIG. 47G

COBW PROTEIN

FIRST RESIDUE = 1
LAST RESIDUE = 354

			NUMBER	NO.%	WEIGHT	WEIGHT %
1	PHE	F	10	2.82	1470.68	3.86
2	LEU	L	32	9.04	3618.69	9.50
3	ILE	I	28	7.91	3166.35	8.31
4	MET	M	7	1.98	917.28	2.41
5	VAL	V	28	7.91	2773.92	7.28
6	SER	S	12	3.39	1044.38	2.74
7	PRO	P	11	3.11	1067.58	2.80
8	THR	T	21	5.93	2122.00	5.57
9	ALA	A	41	11.58	2912.52	7.64
10	TYR	Y	2	0.56	326.13	0.86
11	*	*	0	0.00	0.00	0.00
12	HIS	H	10	2.82	1370.59	3.60
13	GLN	Q	6	1.69	768.35	2.02
14	ASN	N	11	3.11	1254.47	3.29
15	LYS	K	15	4.24	1921.42	5.04
16	ASP	D	36	10.17	4140.97	10.87
17	GLU	E	27	7.63	3484.15	9.15
18	CYS	C	5	1.41	515.05	1.35
19	TRP	W	2	0.56	372.16	0.98
20	ARG	R	20	5.65	3122.02	8.19
21	GLY	G	30	8.47	1710.64	4.49
22	-	-	0	0.00	0.00	0.00

RESIDUES = 354
MOLECULAR WEIGHT (MONOISOTOPIC) = 38097.4258
MOLECULAR WEIGHT (AVERAGE) = 38121.1055
INDEX OF POLARITY (%) = 44.63
ISOELECTRIC POINT = 4.90
OD 260 (1mg/ml) = 0.268 OD 280 (1mg/ml) = 0.354

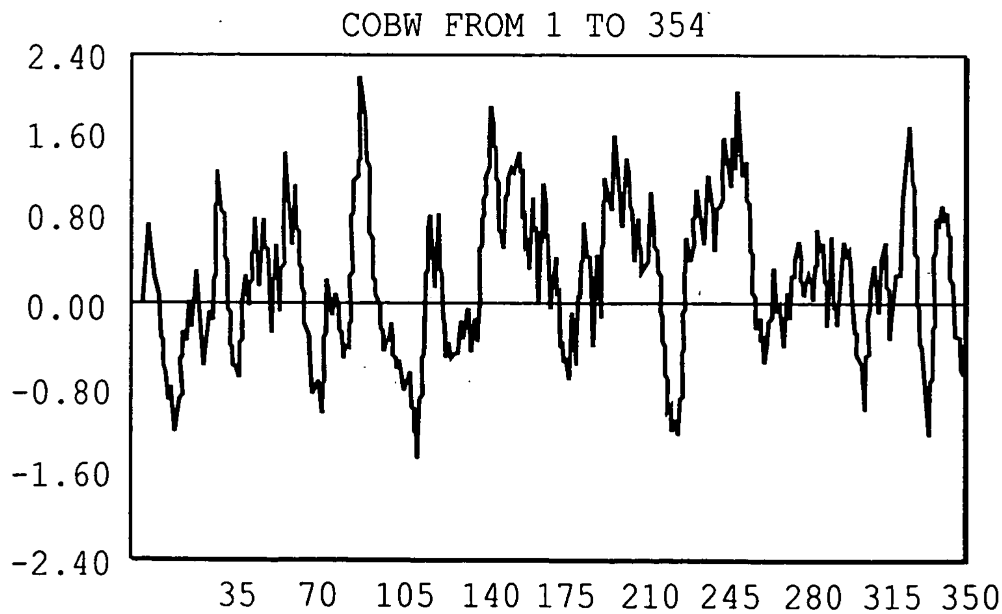


FIG. 47H

13144-BP SEQUENCE FROM 5060 TO 8887 <u>cobN</u> GENE

M H L L L A Q K G T I A D G N E A I D L G Q T P A

ATGCATCTGCTTCTCGCCCAGAAAGGAACGATCGCCGACGGCAACGAGGCGATCGACCTTGGGCAAACGCCGGCC

5060 5070 5080 5090 5100 5110 5120 5130

D I L F L S A A D T E L S S I A A A H G R R D G G

GATATCCTTTTCCTATCGGCCGCCGACACCGAGCTCTCCTCGATCGCCGCGGCTCACGGCCGACGCGACGGAGGC

5135 5145 5155 5165 5175 5185 5195 5205

L S L R I A S L M S L M H P M S V D T Y V E R T A

TTGAGCCTGCGCATCGCCAGCCTGATGAGCCTGATGCACCCGATGTCGGTCGACACTTACGTCGAGCGCACGGCG

5210 5220 5230 5240 5250 5260 5270 5280

R H A K L I V V R P L G G A S Y F R Y L L E A L H

CGTCACGCCAAGCTGATCGTCGTCCGGCCGCTCGGTGGCGCCAGCTATTTCCGTTATCTGCTGGAAGCCCTGCAT

5285 5295 5305 5315 5325 5335 5345 5355

A A A V T H R F E I A V L P G D D K P D P G L E P

GCGGCTGCCGTCACCCATCGTTTCGAGATCGCGGTTCTGCCGGGTGACGACAAGCCGGATCCGGGGCTGGAGCCT

5360 5370 5380 5390 5400 5410 5420 5430

F S T V A A D D R Q R L W A Y F T E G G S D N A G

TTCTCCACCGTCGCAGCCGACGACCGCCAGCGCCTTTGGGCTTACTTCACCGAAGGCGGCTCGGACAATGCCGGG

5435 5445 5455 5465 5475 5485 5495 5505

L F L D Y A A A L V T G A E K P Q P A K P L L K A

CTGTTTCTCGACTATGCGGCCGCACTGGTCACAGGTGCGGAGAAGCCGCAGCCGGCAAAGCCCCTGTTGAAGGCC

5510 5520 5530 5540 5550 5560 5570 5580

G I W W P G A G V I G V S E W Q S L V Q G R M V A

GGCATCTGGTGGCCGGGTGCTGGTGTGATCGGCGTCAGCGAATGGCAGTCCCTTGTTCAGGGACGGATGGTAGCG

5585 5595 5605 5615 5625 5635 5645 5655

R E G F E P P T V G I C F Y R A L V Q S G E T R P

AGGGAGGGATTCGAACCCCCGACGGTCGGGATCTGCTTTTACCGCGCGCTCGTGCAGAGTGGCGAGACACGGCCT

5660 5670 5680 5690 5700 5710 5720 5730

V E A L I D A L E A E G V R A L P V F V S S L K D

GTGGAGGCGCTGATCGATGCGCTGGAGGCTGAAGGTGTGCGGGCACTGCCGGTGTTTGTCTCAAGCCTCAAGGAT

5735 5745 5755 5765 5775 5785 5795 5805

A V S V G T L Q A I F S E A A P D V V M N A T G F

GCCGTTTCCGTCGGCACGCTGCAGGCGATTTTTTCCGAGGCCGCACCCGACGTGGTGATGAACGCCACTGGCTTT

5810 5820 5830 5840 5850 5860 5870 5880

A V S S P G A D R Q P T V L E S T G A P V L Q V I

GCGGTCTCGTCGCCCGGTGCCGACCGTCAGCCGACGGTGCTGGAATCGACCGGTGCGCCGGTGCTGCAGGTGATT

5885 5895 5905 5915 5925 5935 5945 5955

FIG. 47I

```
  F  S  G  S  S  R  A  Q  W  E  T  S  P  Q  G  L  M  A  R  D  L  A  M  N  V
   TTCTCCGGCTCGTCGCGGGCGCAATGGGAAACGTCGCCGCAGGGGCTGATGGCGCGCGACCTCGCCATGAACGTG
5960      5970      5980      5990      6000      6010      6020      6030
  A  L  P  E  V  D  G  R  I  L  A  R  R  V  S  F  K  A  A  S  I  Y  D  A  K
   GCACTCCCCGAAGTCGATGGCCGCATCCTTGCGCGCCGTCTCCTTCAAGGCGGCGTCGATCTATGACGCCAAG
6035      6045      6055      6065      6075      6085      6095      6105
  V  E  A  N  I  V  G  H  E  P  L  E  G  R  V  R  F  A  A  D  L  A  V  N  W
   GTGGAGGCCAATATCGTCGGCCATGAGCCGCTCGAAGGCCGGGTGCGCTTTGCCGCTGATCTTGCCGTCAACTGG
6110      6120      6130      6140      6150      6160      6170      6180
  A  N  V  R  R  A  E  P  A  E  R  R  I  A  I  V  M  A  N  Y  P  N  R  D  G
   GCGAACGTGCGCCGGGCAGAGCCCGCCGAGCGCCGTATTGCCATCGTCATGGCCAACTATCCGAACCGCGACGGT
6185      6195      6205      6215      6225      6235      6245      6255
  R  L  G  N  G  V  G  L  D  T  P  A  G  T  V  E  V  L  S  A  M  A  R  E  G
   CGCCTCGGCAACGGTGTCGGGCTCGACACGCCGGCCGGTACCGTCGAGGTGCTTAGCGCCATGGCGCGGGAAGGC
6260      6270      6280      6290      6300      6310      6320      6330
  Y  A  V  G  E  V  P  A  D  G  D  A  L  I  R  F  L  M  A  G  P  T  N  A  A
   TATGCGGTCGGTGAGGTTCCCGCCGATGGCGACGCGCTGATCCGCTTTCTGATGGCCGGGCCGACCAATGCGGCG
6335      6345      6355      6365      6375      6385      6395      6405
  S  H  D  R  E  I  R  E  R  I  S  L  N  D  Y  K  T  F  F  D  S  L  P  K  Q
   AGCCATGACCGTGAAATCCGCGAGCGTATTTCGCTGAACGATTACAAAACGTTCTTCGATTCGCTTCCGAAACAG
6410      6420      6430      6440      6450      6460      6470      6480
  I  K  D  E  V  A  G  R  W  G  V  P  E  A  D  P  F  F  L  D  G  A  F  A  L
   ATAAAGGATGAAGTTGCCGGTCGCTGGGGCGTGCCGGAGGCCGATCCCTTTTTCCTCGATGGCGCCTTCGCGCTG
6485      6495      6505      6515      6525      6535      6545      6555
  P  L  A  R  F  G  E  V  I  V  G  I  Q  P  A  R  G  Y  N  I  D  P  K  E  S
   CCGCTCGCCCGCTTCGGCGAGGTGATCGTCGGCATCCAACCGGCGCGCGGCTACAACATCGATCCGAAGGAAAGC
6560      6570      6580      6590      6600      6610      6620      6630
  Y  H  S  P  D  L  V  P  P  H  G  Y  L  A  F  Y  A  F  L  R  Q  Q  F  G  A
   TACCATTCCCCGGACCTCGTGCCGCCGCATGGCTATCTCGCCTTCTACGCCTTCCTGCGCCAGCAGTTCGGAGCG
6635      6645      6655      6665      6675      6685      6695      6705
  Q  A  I  V  H  M  G  K  H  G  N  L  E  W  L  P  G  K  A  L  A  L  S  E  T
   CAGGCGATCGTCCACATGGGCAAGCACGGCAATCTCGAATGGCTGCCGGGCAAGGCGCTGGCGCTGTCGGAAACC
6710      6720      6730      6740      6750      6760      6770      6780
  C  Y  P  E  A  I  F  G  P  L  P  H  I  Y  P  F  I  V  N  D  P  G  E  G  T
   TGCTATCCCGAAGCGATCTTCGGGCCGCTGCCGCACATCTATCCCTTCATCGTCAACGATCCGGGCGAAGGTACG
6785      6795      6805      6815      6825      6835      6845      6855
```

FIG. 47J

```
    Q  A  K  R  R  T  S  A  V  I  I  D  H  L  T  P  P  L  T  R  A  E  S  Y  G
    CAGGCCAAGCGCCGCACCAGCGCCGTCATCATCGACCACCTGACCCCGCCCTTGACGCGCGCCGAATCCTACGGC
6860      6870      6880      6890      6900      6910      6920      6930
    P  L  K  D  L  E  A  L  V  D  E  Y  Y  D  A  A  G  G  D  P  R  R  L  R  L
    CCGCTCAAGGATCTGGAAGCGCTCGTCGACGAATATTACGACGCCGCCGGCGGTGATCCGCGCCGCCTCAGGCTG
6935      6945      6955      6965      6975      6985      6995      7005
    L  S  R  Q  I  L  D  L  V  R  D  I  G  L  D  S  D  A  G  I  D  R  G  D  S
    CTCAGCCGCCAGATCCTCGATCTCGTGCGCGACATCGGCCTCGACAGCGACGCAGGCATCGACAGGGGCGACAGC
7010      7020      7030      7040      7050      7060      7070      7080
    D  D  K  A  L  E  K  L  D  A  Y  L  C  D  L  K  E  M  Q  I  R  D  G  L  H
    GACGACAAGGCGCTGGAAAAGCTCGACGCCTATCTCTGCGACCTCAAGGAAATGCAGATCCGCGACGGCCTGCAC
7085      7095      7105      7115      7125      7135      7145      7155
    I  F  G  V  A  P  E  G  R  L  L  T  D  L  T  V  A  L  A  R  V  P  R  G  L
    ATCTTCGGCGTTGCGCCGGAAGGGCGGTTGTTGACGGACCTCACCGTAGCGCTGGCGCGCGTGCCCCGAGGTCTC
7160      7170      7180      7190      7200      7210      7220      7230
    G  E  G  G  D  Q  S  L  Q  R  A  I  A  A  D  A  G  L  R  G  F  A  I  P  T
    GGCGAGGGCGGCGACCAGAGCCTGCAGCGGGCGATCGCAGCGGATGCGGGGCTGCGTGGGTTTGCTATTCCCACC
7235      7245      7255      7265      7275      7285      7295      7305
    S  A  G  G  N  P  A  R  D  A  Q  P  F  D  P  L  D  C  V  M  S  D  T  W  T
    TCGGCGGGGGGCAACCCCGCACGCGACGCCCAACCCTTCGACCCGCTCGACTGCGTCATGTCCGACACCTGGACA
7310      7320      7330      7340      7350      7360      7370      7380
    G  P  K  P  S  I  L  A  D  L  S  D  A  P  W  R  T  A  G  D  T  V  E  R  I
    GGCCCGAAACCGTCCATCCTCGCTGACCTCTCGGACGCCCCCTGGCGCACCGCCGGCGATACGGTCGAGCGCATC
7385      7395      7405      7415      7425      7435      7445      7455
    E  L  L  A  A  N  L  V  S  G  E  L  A  C  P  D  H  W  A  N  T  R  A  V L
    GAGTTGCTTGCCGCAAATCTCGTGTCGGGTGAACTGGCTTGCCCGGACCACTGGGCCAACACCCGCGCCGTGCTC
7460      7470      7480      7490      7500      7510      7520      7530
    G  E  I  E  T  R  L  K  P  S  I  S  N  S  G  A  A  E  M  T  G  F  L  T G
    GGCGAAATCGAAACGCGCCTGAAGCCGTCGATTTCAAACTCGGGTGCCGCCGAGATGACCGGCTTCCTCACCGGT
7535      7545      7555      7565      7575      7585      7595      7605
    L  S  G  R  F  V  A  P  G  P  S  G  A  P  T  R  G  R  P  D  V  L  P  T G
    CTCAGCGGCCGCTTCGTCGCCCCCGGTCCATCGGGCGCGCCGACGCGCGGCCGGCCGGATGTGTTGCCGACGGGG
7610      7620      7630      7640      7650      7660      7670      7680
    R  N  F  Y  S  V  D  S  R  A  V  P  T  P  A  A  Y  E  L  G  K  K  S  A E
    CGCAATTTCTACTCGGTCGACAGCCGCGCCGTGCCGACGCCGGCGGCTTACGAGCTTGGCAAGAAATCGGCCGAG
7685      7695      7705      7715      7725      7735      7745      7755
```

FIG. 47K

```
  L  L  I  R  R  Y  L  Q  D  H  G  E  W  P  S  S  F  G  L  T  A  W  G  T  A
   CTTCTGATCCGCCGCTACCTGCAGGACCATGGCGAATGGCCGTCCTCCTTTGGCCTGACCGCCTGGGGCACGGCG
7760      7770      7780      7790      7800      7810      7820      7830
  N  M  R  T  G  G  D  D  I  A  Q  A  L  A  L  I  G  A  K  P  T  W  D  M  V
   AACATGCGCACCGGCGGCGACGACATCGCCCAGGCCCTGGCGCTGATCGGCGCCAAGCCCACCTGGGACATGGTC
7835      7845      7855      7865      7875      7885      7895      7905
  S  R  R  V  M  G  Y  E  I  V  P  L  A  V  L  G  R  P  R  V  D  V  T  L  R
   TCTCGCCGGGTGATGGGCTACGAGATCGTGCCGCTCGCAGTCCTCGGCCGCCCACGCGTCGACGTGACCTTGCGC
7910      7920      7930      7940      7950      7960      7970      7980
  I  S  G  F  F  R  D  A  F  P  D  Q  I  A  L  F  D  K  A  I  R  A  V  A  L
   ATTTCCGGCTTCTTCCGCGATGCCTTCCCGGACCAGATCGCGCTCTTCGACAAGGCGATCCGCGCCGTCGCGCTG
7985      7995      8005      8015      8025      8035      8045      8055
  E  E  D  D  A  D  N  M  I  A  A  R  M  R  A  E  S  R  R  L  E  A  E  G  V
   GAGGAAGACGATGCCGACAACATGATCGCCGCACGCATGCGGGCGGAAAGCCGGCGGCTGGAGGCCGAAGGCGTG
8060      8070      8080      8090      8100      8110      8120      8130
  E  A  A  E  A  A  R  R  A  S  Y  R  V  F  G  R  K  P  G  A  Y  G  A  A  L
   GAAGCCGCCGAGGCCGCGCGTCGCGCCTCCTACCGCGTCTTTGGCGCAAAGCCCGGTGCCTATGGCGCCGCCCTG
8135      8145      8155      8165      8175      8185      8195      8205
  Q  A  L  I  D  E  K  G  W  E  T  K  A  D  L  A  E  A  Y  L  T  W  G  A  Y
   CAGGCGCTGATCGACGAGAAGGGCTGGGAAACCAAAGCAGATCTCGCCGAGGCCTATCTTACCTGGGGCGCCTAT
8210      8220      8230      8240      8250      8260      8270      8280
  A  Y  G  A  G  E  E  G  K  A  E  R  D  L  F  E  E  R  L  R  T  I  E  A  V
   GCCTATGGCGCCGGCGAGGAGGGCAAGGCCGAGCGCGATCTTTTCGAGGAGCGCCTGCGCACGATAGAGGCGGTG
8285      8295      8305      8315      8325      8335      8345      8355
  V  Q  N  Q  D  N  R  E  H  D  L  L  D  S  D  D  Y  Y  Q  F  E  G  G  M  S
   GTGCAGAACCAGGACAACCGCGAGCACGATCTGCTCGACAGCGACGACTACTACCAGTTCGAAGGCGGCATGAGC
8360      8370      8380      8390      8400      8410      8420      8430
  A  A  A  E  Q  L  G  G  H  R  P  A  I  Y  H  N  D  H  S  R  P  E  K  P  V
   GCTGCCGCCGAACAGCTCGGCGGTCACCGTCCGGCGATCTACCACAACGACCATTCCCGTCCGGAAAAGCCTGTG
8435      8445      8455      8465      8475      8485      8495      8505
  I  R  S  L  E  E  E  I  G  R  V  V  R  A  R  V  V  N  P  K  W  I  D  G  V
   ATCCGGTCGCTCGAAGAAGAGATCGGCCGCGTGGTCCGGGCCCGCGTCGTCAATCCCAAGTGGATCGATGGCGTC
8510      8520      8530      8540      8550      8560      8570      8580
  M  R  H  G  Y  K  G  A  F  E  I  A  A  T  V  D  Y  M  F  A  F  A  A  T  T
   ATGCGCCACGGATACAAGGGCGCCTTCGAGATCGCTGCCACGGTCGACTACATGTTCGCCTTTGCCGCGACCACG
8585      8595      8605      8615      8625      8635      8645      8655
```

FIG. 47L

```
    G  A  V  R  D  H  H  F  E  A  A  Y  Q  A  F  I  V  D  E  R  V  A  D  F  M
     GGTGCGGTGCGCGACCATCATTTCGAGGCCGCTTATCAGGCGTTCATTGTCGACGAGCGCGTGGCTGACTTCATG
8660      8670      8680      8690      8700      8710      8720      8730
    R  D  K  N  P  A  A  F  A  E  L  A  E  R  L  L  E  A  I  D  R  N  L  W  T
     CGCGACAAGAACCCGGCCGCCTTTGCCGAGCTTGCCGAACGCCTGCTTGAAGCAATCGACCGCAATCTCTGGACG
8735      8745      8755      8765      8775      8785      8795      8805
    P  R  S  N  S  A  R  F  E  L  A  G  I  G  T  A  A  T  R  L  R  A  G  N  E
     CCGCGCTCGAATTCGGCGCGGTTTGAACTTGCCGGCATCGGCACGGCAGCAACCCGGCTTCGTGCCGGCAATGAA
8810      8820      8830      8840      8850      8860      8870      8880
    *    (SEQ ID NO: 49)
   TAG   (SEQ ID NO: 48)
8885
```

FIG. 47M

COBN PROTEIN FIRST RESIDUE = 1
LAST RESIDUE = 1275

			NUMBER	NO.%	WEIGHT	WEIGHT %
1	PHE	F	48	3.76	7059.28	5.12
2	LEU	L	121	9.49	13683.17	9.92
3	ILE	I	60	4.71	6785.04	4.92
4	MET	M	24	1.88	3144.97	2.28
5	VAL	V	82	6.43	8123.61	5.89
6	SER	S	64	5.02	5570.05	4.04
7	PRO	P	76	5.96	7376.01	5.35
8	THR	T	53	4.16	5355.53	3.88
9	ALA	A	180	14.12	12786.68	9.27
10	TYR	Y	35	2.75	5707.22	4.14
11	*	*	0	0.00	0.00	0.00
12	HIS	H	24	1.88	3289.41	2.38
13	GLN	Q	32	2.51	4097.87	2.97
14	ASN	N	30	2.35	3421.29	2.48
15	LYS	K	34	2.67	4355.23	3.16
16	ASP	D	90	7.06	10352.42	7.50
17	GLU	E	85	6.67	10968.62	7.95
18	CYS	C	5	0.39	515.05	0.37
19	TRP	W	18	1.41	3349.43	2.43
20	ARG	R	99	7.76	15454.01	11.20
21	GLY	G	115	9.02	6557.47	4.75
22	-	-	0	0.00	0.00	0.00

RESIDUES = 1275
MOLECULAR WEIGHT (MONOISOTOPIC) = 137970.5000
MOLECULAR WEIGHT (AVERAGE) = 138055.8594
INDEX OF POLARITY (%) = 40.08
ISOELECTRIC POINT = 5.42
OD 260 (1mg/ml) = 0.693 OD 280 (1mg/ml) = 1.027

COBN FROM 1 TO 1275

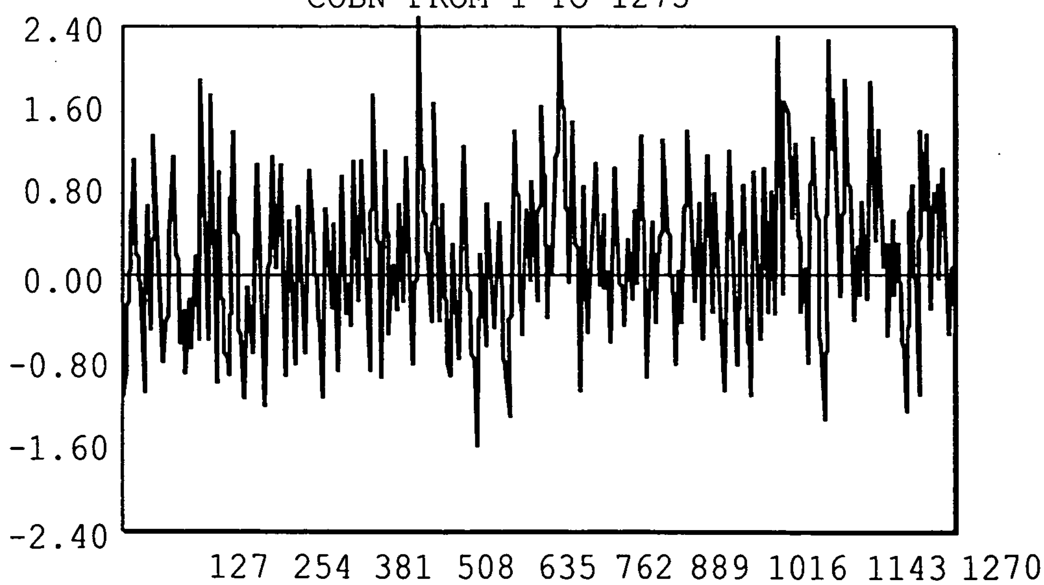


FIG. 47N

13144-BP SEQUENCE 9034 TO 9678 cobO GENE

```
      M  S  D  E  T  T  V  G  G  E  A  P  A  E  K  D  D  A  R  H  A  M  K  M  A
      ATGAGCGACGAGACGACAGTAGGCGGCGAAGCCCCGGCCGAGAAGGACGATGCCCGCCACGCCATGAAGATGGCG
9034       9044      9054      9064      9074      9084      9094      9104
      K  K  K  A  A  R  E  K  I  M  A  T  K  T  D  E  K  G  L  I  I  V  N  T  G
      AAGAAGAAGGCAGCACGCGAAAAGATCATGGCGACGAAGACCGACGAGAAGGGTCTGATCATCGTCAACACCGGC
9109       9119      9129      9139      9149      9159      9169      9179
      K  G  K  G  K  S  T  A  G  F  G  M  I  F  R  H  I  A  H  G  M  P  C  A  V
      AAAGGCAAGGGCAAGTCGACCGCCGGCTTCGGCATGATCTTCCGCCATATCGCCCACGGCATGCCCTGCGCCGTC
9184       9194      9204      9214      9224      9234      9244      9254
      V  Q  F  I  K  G  A  M  A  T  G  E  R  E  L  I  E  K  H  F  G  D  V  C  Q
      GTGCAGTTCATCAAGGGTGCGATGGCAACCGGCGAGCGCGAGTTGATCGAGAAGCATTTCGGCGATGTCTGCCAG
9259       9269      9279      9289      9299      9309      9319      9329
      F  Y  T  L  G  E  G  F  T  W  E  T  Q  D  R  A  R  D  V  A  M  A  E  K  A
      TTCTACACGCTCGGCGAGGGCTTCACCTGGGAAACGCAGGATCGCGCCCGCGATGTTGCGATGGCTGAAAAGGCC
9334       9344      9354      9364      9374      9384      9394      9404
      W  E  K  A  K  E  L  I  R  D  E  R  N  S  M  V  L  L  D  E  I  N  I  R  L
      TGGGAGAAGGCGAAGGAACTGATCCGTGACGAGCGCAACTCGATGGTGCTGCTCGACGAGATCAACATTGCTCTG
9409       9419      9429      9439      9449      9459      9469      9479
      R  Y  D  Y  I  D  V  A  E  V  V  R  F  L  K  E  E  K  P  H  M  T  H  V  V
      CGCTACGACTACATCGACGTCGCCGAAGTGGTGCGCTTCCTGAAGGAAGAAAAGCCGCACATGACGCATGTGGTG
9484       9494      9504      9514      9524      9534      9544      9554
      L  T  G  R  N  A  K  E  D  L  I  E  V  A  D  L  V  T  E  M  E  L  I  K  H
      CTCACCGGCCGCAACGCGAAAGAAGACCTGATCGAAGTCGCCGATCTCGTCACTGAGATGGAGCTGATCAAGCAT
9559       9569      9579      9589      9599      9609      9619      9629
      P  F  R  S  G  I  K  A  Q  Q  G  V  E  F  *        (SEQ ID NO: 51)
      CCGTTCCGTTCCGGCATCAAGGCGCAGCAGGGCGTGGAGTTCTGA      (SEQ ID NO: 50)
9634       9644      9654      9664      9674
```

FIG. 47O

COBO PROTEIN

FIRST RESIDUE = 1
LAST RESIDUE = 214

			NUMBER	NO.%	WEIGHT	WEIGHT %
1	PHE	F	9	4.21	1323.62	5.51
2	LEU	L	12	5.61	1357.01	5.65
3	ILE	I	14	6.54	1583.18	6.59
4	MET	M	11	5.14	1441.45	6.00
5	VAL	V	15	7.01	1486.03	6.19
6	SER	S	4	1.87	348.13	1.45
7	PRO	P	4	1.87	388.21	1.62
8	THR	T	13	6.07	1313.62	5.47
9	ALA	A	23	10.75	1633.85	6.80
10	TYR	Y	3	1.40	489.19	2.04
11	*	*	0	0.00	0.00	0.00
12	HIS	H	7	3.27	959.41	4.00
13	GLN	Q	5	2.34	640.29	2.67
14	ASN	N	4	1.87	456.17	1.90
15	LYS	K	21	9.81	2689.99	11.20
16	ASP	D	13	6.07	1495.35	6.23
17	GLU	E	23	10.75	2967.98	12.36
18	CYS	C	2	0.93	206.02	0.86
19	TRP	W	2	0.93	372.16	1.55
20	ARG	R	12	5.61	1873.21	7.80
21	GLY	G	17	7.94	969.36	4.04
22	-	-	0	0.00	0.00	0.00

RESIDUES = 214
MOLECULAR WEIGHT (MONOISOTOPIC) = 24012.2500
MOLECULAR WEIGHT (AVERAGE) = 24027.6973
INDEX OF POLARITY (%) = 47.66
ISOELECTRIC POINT = 6.94
OD 260 (1mg/ml) = 0.443 OD 280 (1mg/ml) = 0.612

COBO FROM 1 TO 214

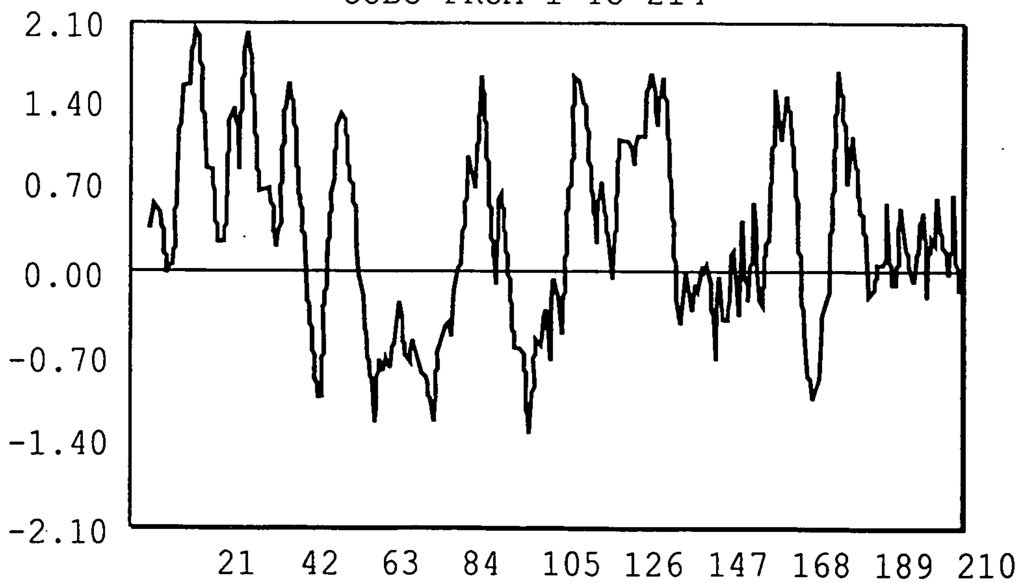


FIG. 47P

NH$_2$-TERMINAL SEQUENCE OF SUMT OF M. ivanovii

VVYLVGAGPGDPELITLKAVNVLK-ADVVL (AMINO ACID FRAGMENT 2-31 OF SEQ ID NO: 54)
923 946

SENSE OLIGONUCLEOTIDE 946 (27-mer)

```
                 P   G   D   P   E   L     (AMINO ACIDS 10-15 OFSEQ ID NO: 54)
5′ CGCGGAATTC CCA GGA GAT CCA GAA CT 3′   (SEQ ID NO: 56)
        EcoRI  T   T   C   T   G
               C   C       C
               G   G       G
```

SENSE OLIGONUCLEOTIDE 923 (27-mer)

```
                 V   Y   L   V   G   A     (AMINO ACIDS 3-8 OF SEQ ID NO: 54)
5′ CGCGGAATTC GTA TAT CTA GTA GGA GC 3′   (SEQ ID NO: 57)
        EcoRI  G   C   T   T   T
                           G
```

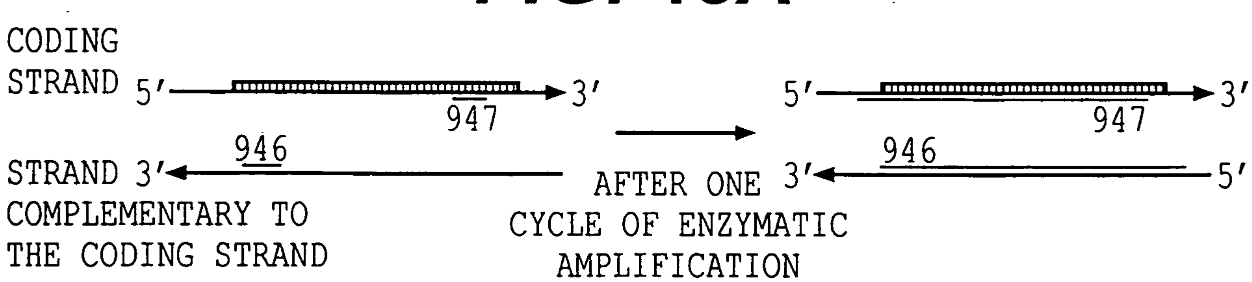
NH$_2$-TERMINAL SEQUENCE OF A FRAGMENT DERIVED FROM A TRYPTIC DIGESTION OF M. ivanovii SUMT

IITGTLENIAGK (AMINO ACIDS 201-212 OF SEQ ID NO: 54)
947

ANTISENSE OLIGONUCLEOTIDE 947 (25-mer)

```
                N   E   L   T   G         (CO2→NH2 ORIENTATION OF AMINO
5′ CGCGAAGCTT GTT TTC TAG AGT ACC 3′      ACIDS 207-203 OF SEQ ID NO: 54)
      HindIII A   C   A   T   T           (SEQ ID NO: 58)
                          G   C
                              G
```

FIG. 48A



M. ivanovii SUMT STRUCTURAL GENE (SEQ ID NO: 54)

FIG. 48B

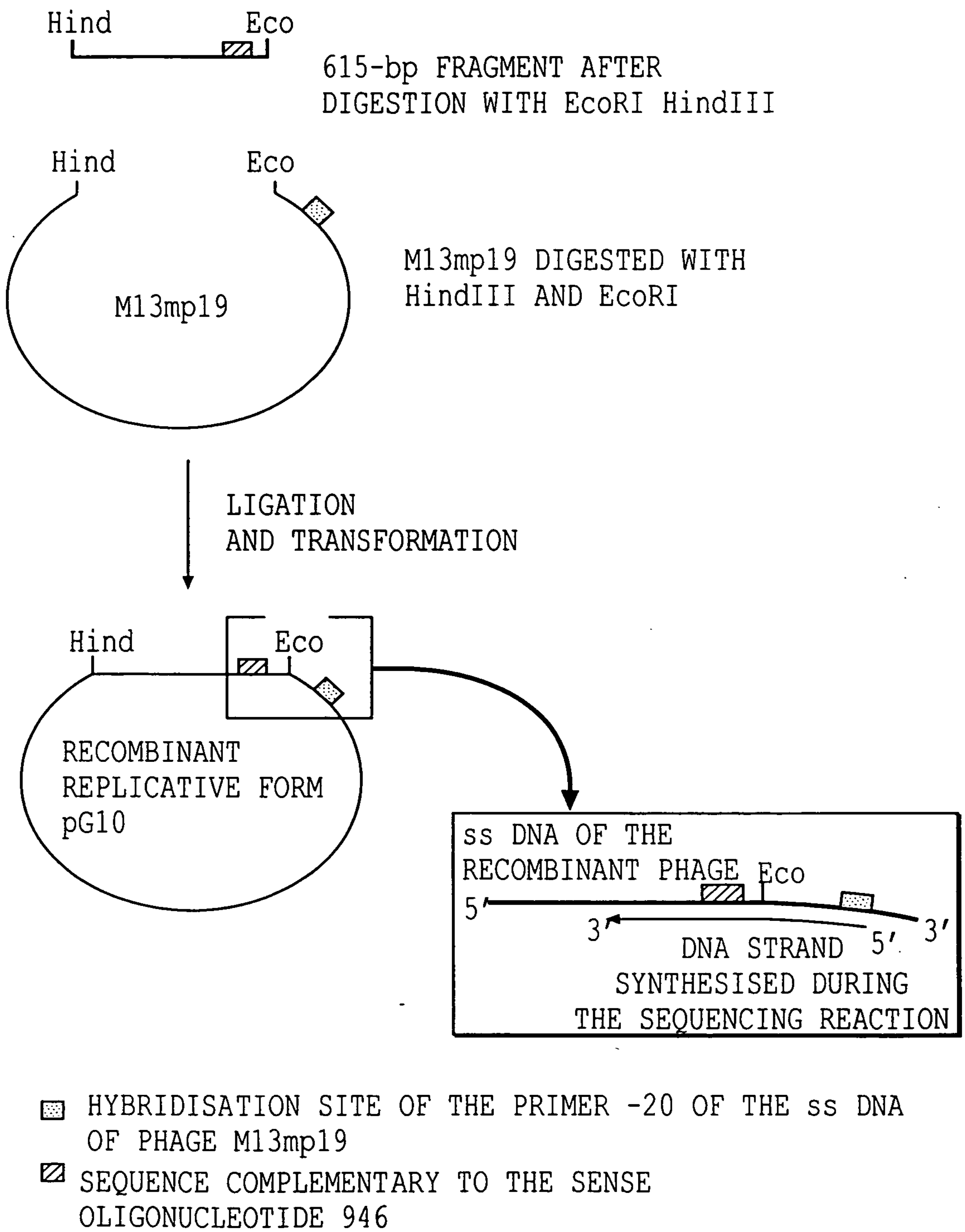

Hind
Eco
615-bp FRAGMENT AFTER DIGESTION WITH EcoRI HindIII
Hind
Eco
M13mp19
M13mp19 DIGESTED WITH HindIII AND EcoRI
LIGATION AND TRANSFORMATION
Hind
Eco
RECOMBINANT REPLICATIVE FORM pG10
ss DNA OF THE RECOMBINANT PHAGE
Eco
5'
3'
3'
5'
DNA STRAND SYNTHESISED DURING THE SEQUENCING REACTION
HYBRIDISATION SITE OF THE PRIMER -20 OF THE ss DNA OF PHAGE M13mp19
SEQUENCE COMPLEMENTARY TO THE SENSE OLIGONUCLEOTIDE 946

FIG. 49

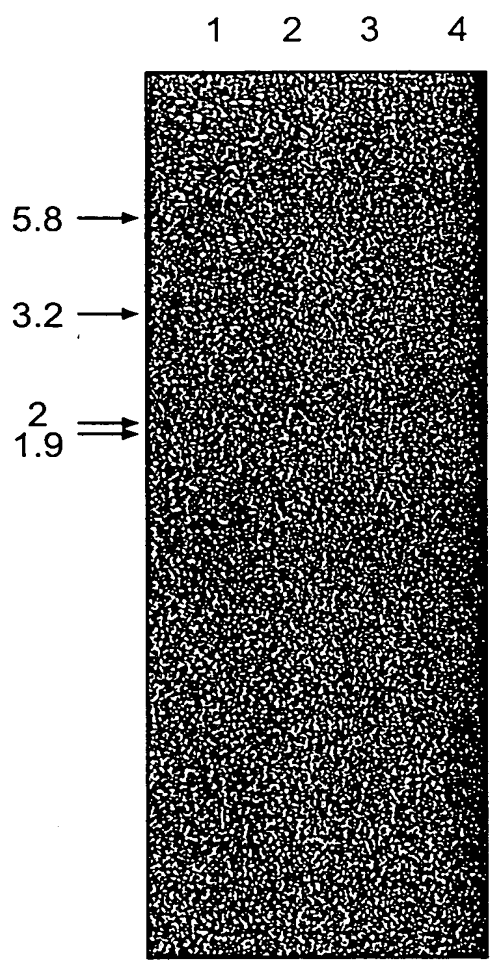


FIG. 50

```
        10         20         30         40         50         60
CCATAATTCT TTTATAATTT AAACGGTGAA CACATGGTAG TTTATTTAGT AGGTGCGGGT
GGTATTAAGA AAATATTAAA TTTGCCACTT GTGTACCATC AAATAAATCA TCCACGCCCA

        70         80         90        100        110        120
CCAGGAGATC CCGAACTTAT CACTCTCAAA GCTGTAAACG TGTTAAAAAA AGCGGATGTT
GGTCCTCTAG GGCTTGAATA GTGAGAGTTT CGACATTTGC ACAATTTTTT TCGCCTACAA

       130        140        150        160        170        180
GTACTGTACG ACAAACCTGC AAATGAAGAA ATTTTAAAGT ATGCTGAAGG TGCAAAACTA
CATGACATGC TGTTTGGACG TTTACTTCTT TAAAATTTCA TACGACTTCC ACGTTTTGAT

       190        200        210        220        230        240
ATATATGTCG GAAAACAAGC AGGACATCAT TACAAATCTC AAAATGAAAT CAATACTCTT
TATATACAGC CTTTTGTTCG TCCTGTAGTA ATGTTTAGAG TTTTACTTTA GTTATGAGAA

       250        260        270        280        290        300
CTTGTTGAAG AAGCAAAAGA AAATGATTTA GTAGTACGCC TTAAAGGTGG AGACCCCTTT
GAACAACTTC TTCGTTTTCT TTTACTAAAT CATCATGCGG AATTTCCACC TCTGGGGAAA

       310        320        330        340        350        360
GTATTTGGAA GAGGAGGCGA GGAAATTCTG GCCCTTGTAG AAGAAGGAAT TGATTTTGAG
CATAAACCTT CTCCTCCGCT CCTTTAAGAC CGGGAACATC TTCTTCCTTA ACTAAAACTC

       370        380        390        400        410        420
TTAGTTCCAG GGGTAACTTC TGCAATTGGA GTTCCAACAA CAATTGGGCT TCCAGTTACT
AATCAAGGTC CCCATTGAAG ACGTTAACCT CAAGGTTGTT GTTAACCCGA AGGTCAATGA

       430        440        450        460        470        480
CATAGAGGTG TTGCAACATC GTTTACAGTT GTTACAGGTC ATGAAGACCC AACAAAATGC
GTATCTCCAC AACGTTGTAG CAAATGTCAA CAATGTCCAG TACTTCTGGG TTGTTTTACG

       490        500        510        520        530        540
AAGAAACAGG TAGGATGGGA CTTTAAAGCA GATACTATTG TAATACTTAT GGGTATTGGA
TTCTTTGTCC ATCCTACCCT GAAATTTCGT CTATGATAAC ATTATGAATA CCCATAACCT

       550        560        570        580        590        600
AATTTAGCTG AAAATACAGC AGAAATTATG AAACATAAAG ATCCTGAAAC TCCAGTTTGT
TTAAATCGAC TTTTATGTCG TCTTTAATAC TTTGTATTTC TAGGACTTTG AGGTCAAACA
```

FIG. 51A

```
       610        620        630        640        650        660
GTAATTGAAA ATGGTACGAT GGAAGGTCAA AGGATAATAA CGGGCACACT GGAAAATATA
CATTAACTTT TACCATGCTA CCTTCCAGTT TCCTATTATT GCCCGTGTGA CCTTTTATAT

       670        680        690        700        710        720
GCTGGAAAGG ATATTAAACC TCCTGCTTTA GTGGTATTGG AAATGTTGTC AATGTTTTTA
CGACCTTTCC TATAATTTGG AGGACGAAAT CACCATAACC TTTACAACAG TTACAAAAAT

       730        740        750        760        770        780
AAGAAATGAA TCAAATCAGT GGCTGATCTA TTAAGAAGGC AATATCATGA ATGGATTAGA
TTCTTTACTT AGTTTAGTCA CCGACTAGAT AATTCTTCCG TTATAGTACT TACCTAATCT

       790        800        810        820        830        840
AGGTAAAAAA ATTGTTATAA CAAGACCTGC TGAAAGGGCT AAAGACTCAG TTGAAATGGT
TCCATTTTTT TAACAATATT GTTCTGGACG ACTTTCCCGA TTTCTGAGTC AACTTTACCA

       850        860        870        880        890        900
AAAATCTTAT GGAGCAGTTC CAATTGTAAC TCCTACAATT GAACTCAAAG ATTCCAAGCC
TTTTAGAATA CCTCGTCAAG GTTAACATTG AGGATGTTAA CTTGAGTTTC TAAGGTTCGG

       910        920        930        940        950        960
AGAAGAAGTG ATAAAATTAT GTAATATGAT AAATGAACCT TGATTGGCCT TATAT
TCTTCTTCAC TATTTTAATA CATTATACTA TTTACTTGGA ACTAACCGGA ATATA
```

FIG. 51B

<u>corA</u> GENE AND CORA PROTEIN (SUMT) OF METHANOBACTERIUM IVANOVII SEQUENCE OF 955-BP FRAGMENT FROM 34 TO 729

```
 M  V  V  Y  L  V  G  A  G  P  G  D  P  E  L  I  T  L  K  A  V  N  V  L  K
ATGGTAGTTTATTTAGTAGGTGCGGGTCCAGGAGATCCCGAACTTATCACTCTCAAAGCTGTAAACGTGTTAAAA
34        44        54        64        74        84        94        104
 K  A  D  V  V  L  Y  D  K  P  A  N  E  E  I  L  K  Y  A  E  G  A  K  L  I
AAAGCGGATGTTGTACTGTACGACAAACCTGCAAATGAAGAAATTTTAAAGTATGCTGAAGGTGCAAAACTAATA
109       119       129       139       149       159       169       179
 Y  V  G  K  Q  A  G  H  H  Y  K  S  Q  N  E  I  N  T  L  L  V  E  E  A  K
TATGTCGGAAAACAAGCAGGACATCATTACAAATCTCAAAATGAAATCAATACTCTTCTTGTTGAAGAAGCAAAA
184       194       204       214       224       234       244       254
 E  N  D  L  V  V  R  L  K  G  G  D  P  F  V  F  G  R  G  G  E  E  I  L  A
GAAAATGATTTAGTAGTACGCCTTAAAGGTGGAGACCCCTTTGTATTTGGAAGAGGAGGCGAGGAAATTCTGGCC
259       269       279       289       299       309       319       329
 L  V  E  E  G  I  D  F  E  L  V  P  G  V  T  S  A  I  G  V  P  T  T  I  G
CTTGTAGAAGAAGGAATTGATTTTGAGTTAGTTCCAGGGGTAACTTCTGCAATTGGAGTTCCAACAACAATTGGG
334       344       354       364       374       384       394       404
 L  P  V  T  H  R  G  V  A  T  S  F  T  V  V  T  G  H  E  D  P  T  K  C  K
CTTCCAGTTACTCATAGAGGTGTTGCAACATCGTTTACAGTTGTTACAGGTCATGAAGACCCAACAAAATGCAAG
409       419       429       439       449       459       469       479
 K  Q  V  G  W  D  F  K  A  D  T  I  V  I  L  M  G  I  G  N  L  A  E  N  T
AAACAGGTAGGATGGGACTTTAAAGCAGATACTATTGTAATACTTATGGGTATTGGAAATTTAGCTGAAAATACA
484       494       504       514       524       534       544       554
 A  E  I  M  K  H  K  D  P  E  T  P  V  C  V  I  E  N  G  T  M  E  G  Q  R
GCAGAAATTATGAAACATAAAGATCCTGAAACTCCAGTTTGTGTAATTGAAAATGGTACGATGGAAGGTCAAAGG
559       569       579       589       599       609       619       629
 I  I  T  G  T  L  E  N  I  A  G  K  D  I  K  P  P  A  L  V  V  L  E  M  L
ATAATAACGGGCACACTGGAAAATATAGCTGGAAAGGATATTAAACCTCCTGCTTTAGTGGTATTGGAAATGTTG
634       644       654       664       674       684       694       704
 S  M  F  L  K  K  *
TCAATGTTTTTAAAGAAATGA
709       719       729
```

FIG. 52A

CORA PROTEIN

			NUMBER	NO. %	WEIGHT	WEIGHT %
1	PHE	F	6	2.60	882.41	3.54
2	LEU	L	22	9.52	2487.85	9.99
3	ILE	I	17	7.36	1922.43	7.72
4	MET	M	6	2.60	786.24	3.16
5	VAL	V	26	11.26	2575.78	10.34
6	SER	S	4	1.73	348.13	1.40
7	PRO	P	12	5.19	1164.63	4.68
8	THR	T	16	6.93	1616.76	6.49
9	ALA	A	16	6.93	1136.59	4.56
10	TYR	Y	5	2.16	815.32	3.27
11	*	*	0	0.00	0.00	0.00
12	HIS	H	5	2.16	685.29	2.75
13	GLN	Q	4	1.73	512.23	2.06
14	ASN	N	9	3.90	1026.39	4.12
15	LYS	K	20	8.66	2561.90	10.29
16	ASP	D	11	4.76	1265.30	5.08
17	GLU	E	21	9.09	2709.89	10.88
18	CYS	C	2	0.87	206.02	0.83
19	TRP	W	1	0.43	186.08	0.75
20	ARG	R	4	1.73	624.40	2.51
21	GLY	G	24	10.39	1368.52	5.50
22	-	-	0	0.00	0.00	0.00

RESIDUES = 231
MOLECULAR WEIGHT (MONOISOTOPIC) = 24900.1855
MOLECULAR WEIGHT (AVERAGE) = 24915.9766
INDEX OF POLARITY (%) = 40.69
ISOELECTRIC POINT = 5.45
OD 260 (1mg/ml) = 0.304 OD 280 (1mg/ml) = 0.462

FIG. 52B

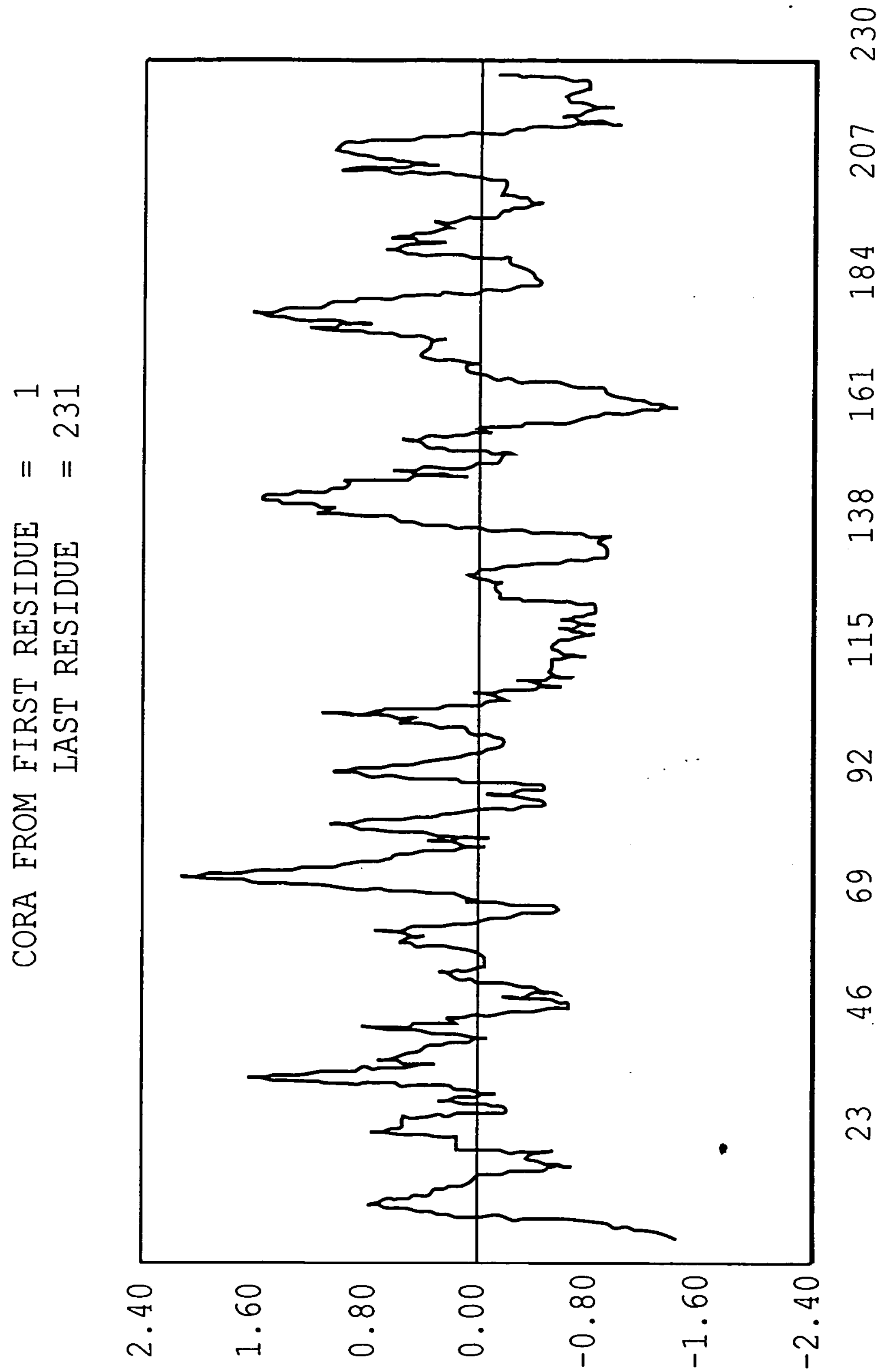

CORA FROM FIRST RESIDUE = 1
LAST RESIDUE = 231
2.40
1.60
0.80
0.00
-0.80
-1.60
-2.40
23
46
69
92
115
138
161
184
207
230

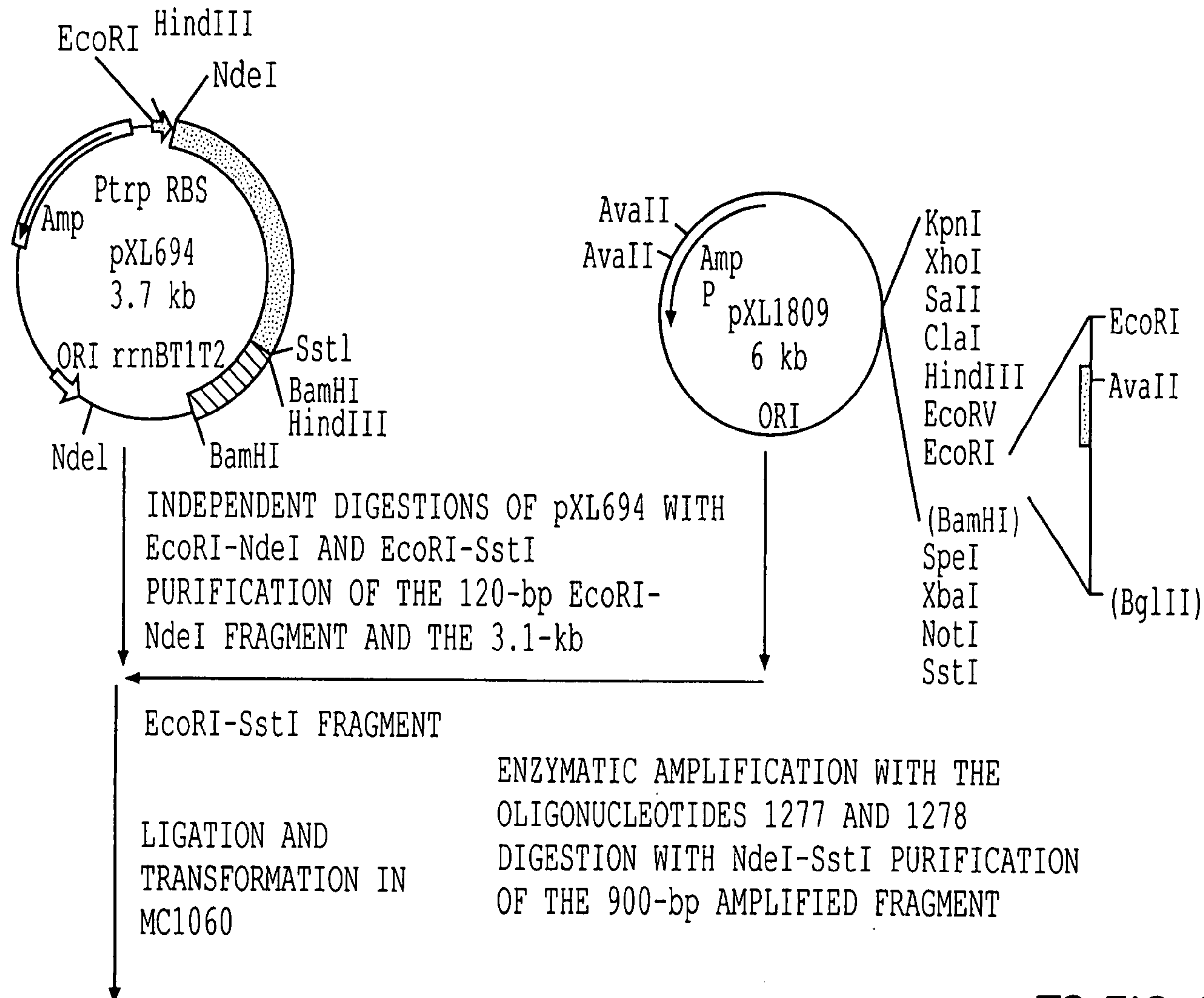
FIG. 52C

```
M. IVANOVII CORA             3 TO 227
P. DENITRIFICANS COBA        17 TO 251

       10        20        30        40         50        60        70
VYLVGAGPGDPELITLKAVNVLKKADVVLYDKPANEEILKYAE-GAKLIYVGKQAGHHYKSQNEINTLLV
=-========= =-== = = =- ===-- =   ==- == =   == = - == -=      = -=   ==
VWLVGAGPGDPGLLTLHAANALRQADVIVHDALVNEDCLKLARPGAVLEFAGKRGGKPSPKQRDISLRLV
  20        30        40        50        60        70        80
     80        90       100       110       120       130       140
EEAKENDLVVRLKGGDPFVFGRGGEEILALVEEGIDFELVPGVTSAIGVPTTIGLPVTHRGVATSFTVVT
= =-   - =================== =-===   - = -===-=-===   -   =-===== =  - = -=
ELARAGNRVLRLKGGDPFVFGRGGEEALTLVEHQVPFRIVPGITAGIGGLAYAGIPVTHREVNHAVTFLT
  90       100       110       120       130       140       150
    150        160          170        180        190        200
GHEDPTKCKKQVGWD-FKADT-IVIL-MGIGNLAENTAEIMKH-KDPETPVCVIENGTMEGQRIITGTL-
==-   -       - =-    - - ---- ===   --    ==---    - =- ==   - =--    = -- -==
GHDSSGLVPDRINWQGIASGSPVIVMYMAMKHIGAITANLIAGGRSPDEPVAFVCNAATPQQAVLETTLA
 160       170       180       190       200       210       220
   210       220
--E-NIAGKDIKPPALVVL-EMLSM
  = --=-   - ===-==- =-- -
RAEADVAAAGLEPPAIVVVGEVVRL
 230       240       250
```

PERCENTAGE OF STRICT HOMOLOGY : 40.4

FIG. 53



TO FIG. 54B

TO FIG. 54B

FIG. 54A

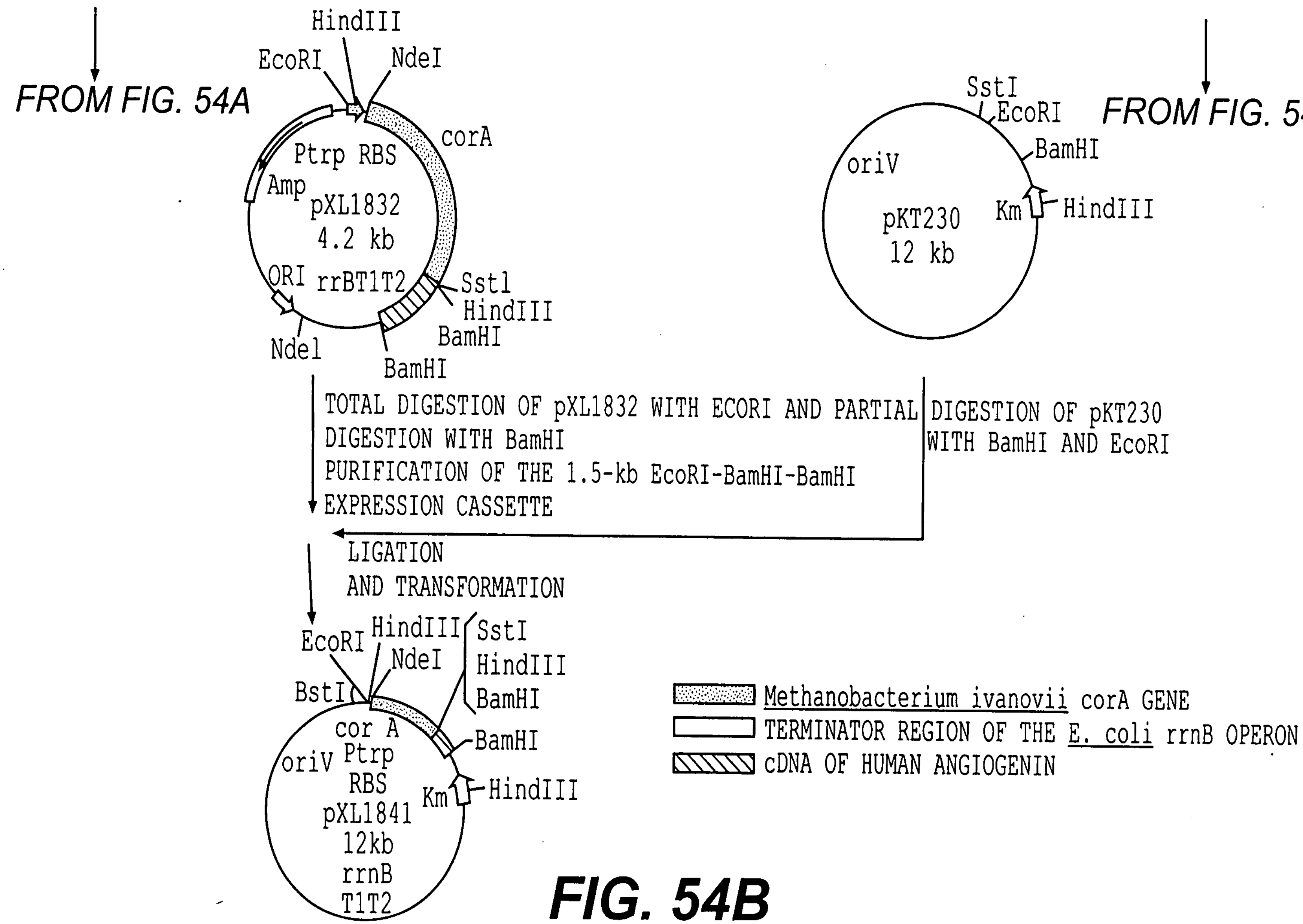

FROM FIG. 54A
HindIII
EcoRI
NdeI
corA
Ptrp RBS
Amp
pXL1832
4.2 kb
ORI
rrBT1T2
Sstl
HindIII
BamHI
Ndel
BamHI
FROM FIG. 54A
SstI
EcoRI
BamHI
oriV
Km
HindIII
pKT230
12 kb
TOTAL DIGESTION OF pXL1832 WITH ECORI AND PARTIAL
DIGESTION WITH BamHI
PURIFICATION OF THE 1.5-kb EcoRI-BamHI-BamHI
EXPRESSION CASSETTE
DIGESTION OF pKT230
WITH BamHI AND EcoRI
LIGATION
AND TRANSFORMATION
EcoRI
HindIII
NdeI
SstI
HindIII
BamHI
BstI
cor A
Ptrp
RBS
oriV
BamHI
Km
HindIII
pXL1841
12kb
rrnB
T1T2
Methanobacterium ivanovii corA GENE
TERMINATOR REGION OF THE E. coli rrnB OPERON
cDNA OF HUMAN ANGIOGENIN

FIG. 54B

PURIFICATION OF PSEUDOMONAS DENITRIFICANS COBINAMIDE KINASE - COBINAMIDEPHOSPHATE GUANYLYL TRANSFERASE

PURIFICATION STEP	VOL (ml)	PROTEIN (mg)	COBINAMIDE KINASE			COBINAMIDEPHOSPHATE GUANYLYL TRANSFERASE	RATIO OF sp. act. 2/1
			sp. act. 1 (U/mg of protein)	YIELD (%)	PURIFICATION FACTOR	sp. act. 2 (U/mg OF PROTEIN)	
CRUDE EXTRACT*	4.5	120	16	-	-	214	13
MONO Q HR 10/10 ELUATE	9.0	8.98	188	88	12	-	-
HYDROXYAPATITE ELUATE	2.0	4.55	325	77	20	3640	11
PHENYL-SUPEROSE ELUATE	2.0	1.51	560	44	35	-	-
MONO Q HR 5/5 ELUATE	3.0	0.90	786	37	49	11282	14

*FROM 1 G OF WET SC510 PXL622 CELLS CULTURED ON PS4 MEDIUM (CAMERON ET AL., 1989) WITHOUT COBALT.

FIG. 55